

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:11:57 ; Search time 3717.85 Seconds  
(without alignments)  
10265.033 Million cell updates/sec

Title: US-10-070-532-1  
Perfect score: 1278  
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgcctgccctga 1278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Match	Length	Query				
	1	751.4	58.8	753	29	AY420885			AY420885 Homo sapi
c	2	732.8	57.3	886	13	BX433093			BX433093 BX433093
	3	719.4	56.3	1740	11	BC035686			BC035686 Homo sapi
c	4	692.8	54.2	790	14	CF147830			CF147830 AGENCOURT
c	5	676.4	52.9	899	13	BX433092			BX433092 BX433092
	6	662.8	51.9	750	29	AY420886			AY420886 Pan trogl
	7	578.6	45.3	3470	11	AK048781			AK048781 Mus muscu
	8	578.6	45.3	3729	11	AK038551			AK038551 Mus muscu
	9	575.4	45.0	726	29	AY420887			AY420887 Mus muscu
	10	567.6	44.4	3153	11	AK079572			AK079572 Mus muscu
	11	521	40.8	1790	11	BC035858			BC035858 Homo sapi
	12	470.4	36.8	1001	9	AL535838			AL535838 AL535838
	13	468.4	36.7	520	13	BQ269289			BQ269289 ik23f12.y
	14	437.4	34.2	892	13	BX409735			BX409735 BX409735
	15	393.2	30.8	993	12	BM926746			BM926746 AGENCOURT
c	16	386.8	30.3	625	13	BQ285933			BQ285933 ik23f12.x
	17	376.2	29.4	543	13	BX119589			BX119589 BX119589
	18	367	28.7	788	14	CF147829			CF147829 AGENCOURT
c	19	336.2	26.3	1013	9	AL535837			AL535837 AL535837
	20	330.8	25.9	382	12	BQ042116			BQ042116 sheep1 Sh
c	21	296	23.2	525	12	BI133700			BI133700 UI-M-BH3-
	22	285.4	22.3	635	12	BM939496			BM939496 UI-M-BH3-
	23	265.8	20.8	627	10	BB632359			BB632359 BB632359
	24	265.4	20.8	599	12	BM933820			BM933820 UI-M-BH3-
	25	263.2	20.6	611	13	BY723922			BY723922 BY723922
	26	216.8	17.0	477	12	BM087401			BM087401 500158 MA
	27	206	16.1	552	10	BE863072			BE863072 UI-M-BH0-
	28	202.4	15.8	662	10	BB632883			BB632883 BB632883
	29	199.8	15.6	1073	12	BM920548			BM920548 AGENCOURT
	30	198.4	15.5	245	12	BI976482			BI976482 485407 MA
	31	197.6	15.5	505	10	BB651179			BB651179 BB651179
	32	186.2	14.6	464	13	BY239887			BY239887 BY239887
	33	177	13.8	444	14	R55704			R55704 yg88h10.r1
	34	173.4	13.6	768	13	BX109847			BX109847 BX109847
c	35	167.4	13.1	703	29	CE375359			CE375359 tigr-gss-
	36	163.2	12.8	1290	29	AY411591			AY411591 Homo sapi
	37	162	12.7	721	29	CE235359			CE235359 tigr-gss-
	38	157.8	12.3	1296	29	AY411593			AY411593 Mus muscu
	39	134.6	10.5	257	10	AW427900			AW427900 64510 MAR
c	40	127.2	10.0	1005	28	CC212654			CC212654 CH261-75F
c	41	127.2	10.0	1058	28	CC297061			CC297061 CH261-177
c	42	125.4	9.8	564	13	BU680891			BU680891 UI-CF-EC1
c	43	122.4	9.6	1194	28	CC279941			CC279941 CH261-24C
	44	120.2	9.4	526	29	CG978334			CG978334 CH240_169
	45	120.2	9.4	661	10	BB638470			BB638470 BB638470

## ALIGNMENTS

RESULT 1  
AY420885  
LOCUS AY420885 753 bp DNA linear GSS 17-DEC-2003  
DEFINITION Homo sapiens HCRT1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY420885  
VERSION AY420885.1 GI:39776842  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 753)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 753)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence as made by sequencing genomic exons and ordering them  
based on alignment.  
FEATURES Location/Qualifiers  
source 1. .753  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
gene <1. .>753  
/gene="HCRT1"  
/locus\_tag="HCM7373"  
ORIGIN

Query Match 58.8%; Score 751.4; DB 29; Length 753;  
Best Local Similarity 99.9%; Pred. No. 4.5e-140;  
Matches 752; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585  
|||||  
Db 1 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 60  
Qy 586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645  
|||||  
Db 61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120

Qy 646 CACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705  
 |||  
 Db 121 CACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy 706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765  
 |||  
 Db 181 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy 766 CGGAACTGGAAGCGCCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825  
 |||  
 Db 241 CGGAACTGGAAGCGCCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 300

Qy 826 CCCCAGCCCCGGGCCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885  
 |||  
 Db 301 CCCCAGCCCCGGGCCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 360

Qy 886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945  
 |||  
 Db 361 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 420

Qy 946 GTCCTCAATGTCCTTAAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005  
 |||  
 Db 421 GTCCTCAATGTCCTTAAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 480

Qy 1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065  
 |||  
 Db 481 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 540

Qy 1066 ATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 1125  
 |||  
 Db 541 ATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 600

Qy 1126 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCC 1185  
 |||  
 Db 601 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCC 660

Qy 1186 AGCCACAAGTCCTTGTCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTG 1245  
 |||  
 Db 661 AGCCACAAGTCCTTGTCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTG 720

Qy 1246 GTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 721 GTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 753

# RESULT 2

BX433093/c

LOCUS BX433093 886 bp mRNA linear EST 15-MAY-2003

DEFINITION BX433093 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 CS0DF013YE04 3-PRIME, mRNA sequence.

ACCESSION BX433093

VERSION BX433093.1 GI:30779168

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



REFERENCE 1 (bases 1 to 886)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 151.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0BAI011ZB01\_CS00962\_2&cluster=151.r.  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01\_CS00962\_2.

FEATURES Location/Qualifiers  
source 1. .886  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DF013YE04"  
/tissue\_type="FETAL BRAIN"  
/dev\_stage="fetal"  
/clone\_lib="Homo sapiens FETAL BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

# ORIGIN

Query Match 57.3%; Score 732.8; DB 13; Length 886;  
Best Local Similarity 98.9%; Pred. No. 2.6e-136;  
Matches 737; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

Qy      377 AGGCTGTGTCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 436
          |||
Db      745 AGGCTGTGTCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 686

Qy      437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
          |||
Db      685 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATNC 626

Qy      497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 556
          |||
Db      625 TGGGCATCTGGCCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATGCA 566

Qy      557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 616
          |||
Db      565 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 506

Qy      617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
          |||
Db      505 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 446

```

QY 677 CCCCCTGGGCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 736  
 |||  
 Db 445 CCCCCTGGGCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 386  
 QY 737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGCCCTCAGACCAGCTGG 796  
 |||  
 Db 385 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGCCCTCAGACCAGCTGG 326  
 QY 797 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCCGCGCCTTCCTGGCTG 856  
 |||  
 Db 325 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCCGCGCCTTCCTGGCTG 266  
 QY 857 AAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 916  
 |||  
 Db 265 AAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 206  
 QY 917 TCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTCGGGA 976  
 |||  
 Db 205 TCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTCGGGA 146  
 QY 977 TGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGC 1036  
 |||  
 Db 145 TGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGC 86  
 QY 1037 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTCCTCAGTGGCAAATTCC 1096  
 |||  
 Db 85 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTCCTCAGTGGCAAATTCC 26  
 QY 1097 GGGAGCAGTTTAAGGCTGCCTTCTC 1121  
 |||  
 Db 25 GGGAGCAGTTTAAGGCATCCTTCTC 1

RESULT 3  
 BC035686

LOCUS BC035686 1740 bp mRNA linear HTC 20-SEP-2002

DEFINITION Homo sapiens, Similar to hypocretin (orexin) receptor 1, clone  
 IMAGE:5750551, mRNA.

ACCESSION BC035686

VERSION BC035686.1 GI:23242909

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1740)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 79 Row: m Column: 17  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4557636  
 This clone has the following problem: frame shifted.

#### FEATURES

Location/Qualifiers  
 source 1. .1740  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5750551"  
 /tissue\_type="Lung, Spleen, fetal, pooled"  
 /clone\_lib="NIH\_MGC\_122"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"

#### ORIGIN

Query Match 56.3%; Score 719.4; DB 11; Length 1740;  
 Best Local Similarity 83.5%; Pred. No. 1.7e-133;  
 Matches 909; Conservative 0; Mismatches 1; Indels 179; Gaps 1;

```

Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      506 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 565

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db      566 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 625

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db      626 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGGCC 685

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||
Db      686 CTGGTGGGCAACACGCTG----- 703

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
Db      704 ----- 703

```

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Db 704 ----- 703

Qy 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||

Db 704 -----GGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 746

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||

Db 747 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 806

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 |||

Db 807 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 866

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||

Db 867 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 926

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||

Db 927 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 986

Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||

Db 987 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 1046

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 |||

Db 1047 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC 1106

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||

Db 1107 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 1166

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||

Db 1167 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1226

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||

Db 1227 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1286

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||

Db 1287 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1346

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 |||

Db 1347 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1406

Qy 1081 CTCAGTGGC 1089  
 |||

Db 1407 CTCAGTGGC 1415



```

Db      790 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 731
Qy      643 TACCACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 702
      |||
Db      730 TACCACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 671
Qy      703 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 762
      |||
Db      670 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 611
Qy      763 GTGCGGAAGTGAAGCGCCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 822
      |||
Db      610 GTGCGGAAGTGAAGCGCCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 551
Qy      823 GAGCCCCAGCCCCGGGCCCGCGCCTTCTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 882
      |||
Db      550 GAGCCCCAGCCCCGGGCCCGCGCCTTCTCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 491
Qy      883 AAGACAGCCAAGATGCTGATGGTGGTGTCTGGTCTTCGCCCTCTGCTACCTGCCCATC 942
      |||
Db      490 AAGACAGCCAAGATGCTGATGGTGGTGTCTGGTCTTCGCCCTCTGCTACCTGCCCATC 431
Qy      943 AGCGTCCTCAATGTCCTTAAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 1002
      |||
Db      430 AGCGTCCTCAATGTCCTTAAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 371
Qy      1003 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 1062
      |||
Db      370 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 311
Qy      1063 CCCATCATCTACAACCTTCCTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCC 1122
      |||
Db      310 CCCATCATCTACAACCTTCCTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCC 251
Qy      1123 TGCTGCCTGCCTGGCCTGGGTCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCT 1182
      |||
Db      250 TGCTGCCTGCCTGGCCTGGGCCCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCT 191
Qy      1183 GCCAGCCACAAGTCCTTGTCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCAT 1242
      |||
Db      190 GCCAGCCACAAGTCCTTGTCCTTGAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCAT 131
Qy      1243 GTGGTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 1278
      |||
Db      130 GTGGTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 95

```

RESULT 5

BX433092/c

LOCUS BX433092 899 bp mRNA linear EST 15-MAY-2003

DEFINITION BX433092 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
CS0DF013YE04 3-PRIME, mRNA sequence.

ACCESSION BX433092

VERSION BX433092.1 GI:30779167

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 899)
AUTHORS        Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished (2001)
COMMENT        Contact: Genoscope
                Genoscope - Centre National de Sequencage
                BP 191 91006 EVRY cedex - France
                Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                Library was constructed by Life Technologies, a division of
                Invitrogen. This sequence belongs to sequence cluster 151.r For
                more information about this cluster, see
                http://www.genoscope.cns.fr/
                cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_1&cluster=151.r.
                Contact : Feng Liang Email : fliang@lifetech.com URL :
                http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_1.

FEATURES             Location/Qualifiers
     source            1..899
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CS0DF013YE04"
                        /tissue_type="FETAL BRAIN"
                        /dev_stage="fetal"
                        /clone_lib="Homo sapiens FETAL BRAIN"
                        /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                        was primed with a NotI-oligo(dT) primer. Five prime end
                        enriched, double-strand cDNA was digested with Not I and
                        cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                        vector. Library was not normalized."

ORIGIN

Query Match          52.9%; Score 676.4; DB 13; Length 899;
Best Local Similarity 96.6%; Pred. No. 5.2e-125;
Matches 711; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

Qy      372 TCTACAGGCTGTGTCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCG 431
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      738 TGTAAGNNCTGTGTCTGTTCAGTGGCAGTGCTACTTCTCAGCTTCATCGCCTGGACCCG 679

Qy      432 CTGGTATGCCATC-TGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCT 490
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      678 CTGGTATGCCATCATCCACCCACTATTGTCAAAGAGCACAGCCCGGCGGGCCCGTGGCTC 619

Qy      491 CCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 550
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      618 CCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 559

Qy      551 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 610
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      558 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 499

Qy      611 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 670
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      498 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 439

```

Qy 671 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 730  
 |||  
 Db 438 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 379  
 Qy 731 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGCTGGAAGCGCCCCCTCAGACC 790  
 |||  
 Db 378 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGCTGGAAGCGCCCCCTCAGACC 319  
 Qy 791 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCC 850  
 |||  
 Db 318 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCC 259  
 Qy 851 TGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 910  
 |||  
 Db 258 TGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 199  
 Qy 911 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 970  
 |||  
 Db 198 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 139  
 Qy 971 TCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 1030  
 |||  
 Db 138 TCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 79  
 Qy 1031 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGGCA 1090  
 |||  
 Db 78 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCT-CAACTTCCTCAGGTGCA 20  
 Qy 1091 AATTCCGGGAGCAGTT 1106  
 |||  
 Db 19 AATTCCGGGAGCAGTT 4

# RESULT 6

AY420886

LOCUS AY420886 750 bp DNA linear GSS 17-DEC-2003

DEFINITION Pan troglodytes HCRT1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY420886

VERSION AY420886.1 GI:39776843

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 750)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 750)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,



[illegible]

Qy 1066 ATCATCTACAACCTTCCTCAGTGGCAAATTCGGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 1125  
 |||| |  
 Db 541 ATCANNNACAACCTTCCTCAGTGGCAAATTCGGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 600  
 Qy 1126 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCC 1185  
 |||| |  
 Db 601 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCC 660  
 Qy 1186 AGCCACAAGTCCTTGTCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTG 1245  
 |||| |  
 Db 661 AGCCACAAGTCCTTGTCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTG 720  
 Qy 1246 GTGCTCACCAGCGTCACCACAGTGCTGCCC 1275  
 |||| |  
 Db 721 GTGCTCACCAGCGTCACCACAGTGCTGCCC 750

RESULT 7

AK048781

LOCUS AK048781 3470 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230065B06 product:OREXIN RECEPTOR TYPE 2, full insert sequence.

ACCESSION AK048781

VERSION AK048781.1 GI:26339571

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4-

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3470)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3470  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM\_DB:C230065B06"  
/db\_xref="MGI:2415851"  
/db\_xref="taxon:10090"  
/clone="C230065B06"  
/tissue\_type="cerebellum"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="0 day neonate"

CDS 75. .1457  
/note="unnamed protein product; OREXIN RECEPTOR TYPE 2 (SWISSPROT|P56719, evidence: FASTY, 98.5%ID, 100%length, match=1380)

```

putative"
/codon_start=1
/protein_id="BAC33457.1"
/db_xref="GI:26339572"
/translation="MSSTKLEDSLRRNWSSASELNETQEPFLNPTDYDDEEFLRYLW
REYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNHMRVTVTNYFIVNLSLADVL
VTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVLTLSCIALDRWYAICHPL
MFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSMLPGLANKTTLFTVCDEHWGGEV
YPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQRKWKQQQPVSQPR
GSGQQSKARISAVAAEIKQIRARRKTARMLMVLLVFAICYLPISILNVLKRVFGMFT
HTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSGKFREEFKAAFSCCLGVHHRQGDR
LARGRTSTESRSLTTQISNFDNVSKLSEHVVLTSISTLPAANGAGPLQNWYLOQGV
SSLLSTWLEV"
polyA_signal 3455. .3460
polyA_site 3470
/note="putative"
/note="putative"

```

# ORIGIN

```

Query Match          45.3%;  Score 578.6;  DB 11;  Length 3470;
Best Local Similarity 69.0%;  Pred. No. 3.7e-105;
Matches 826;  Conservative 0;  Mismatches 359;  Indels 12;  Gaps 2;

```

```

Qy      80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     178 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 237

Qy     140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCCCTGGTGGGCAACACGCTGG 199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     238 GGGTCCTGATCGCAGGGTATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG 297

Qy     200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     298 TCTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACAGTCACCAACTACTTCATAGTCA 357

Qy     260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     358 ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG 417

Qy     320 ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     418 ACATCACTGAGACTTGGTTCTTTGGACAGTCCCTCTGTAAGGTCATTTCCTTATTTACAGA 477

Qy     380 CTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     478 CTGTGTGTCAGTGTCTGTGTCTGTTCTTACGTTGAGCTGCATTGCCTTGGACCGATGGTACG 537

Qy     440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGGCGGGCCGCTGGCTCCATCCTGG 499
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     538 CCATTTGTCAACCCTTTGATGTTCAAGAGCACAGCCAAACGGGCTCGAAACAGCATCGTTG 597

Qy     500 GCATCTGGGCTGTGTGCTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     598 TCATCTGGATCGTCTCCTGCATCATAATGATTCTCAAGCCATTGTCATGGAGTGCAGCA 657

Qy     560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

Db      658 GCATGCTCCCTGGCCTAGCCAATAAGACCACCCTCTTTACAGTATGTGATGAACACTGGG 717
Qy      620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC 679
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      718 GCGGTGAAGTTTACCCAAAGATGTACCATATCTGCTTCTTTCTGGTGACATACATGGCAC 777
Qy      680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      778 CTCTGTGTCTTATGATATTGGCTTATCTCCAAATATTCCGTAAACTCTGGTGCCGACAGA 837
Qy      740 TCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGCCCCCTCAGACCAGCTGGGGG 799
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      838 TTCCCGGAACCTTCTTCTGTGGTTCAGAGAAAATGGAAGCAGC-----AGCAGCCGGTTT 891
Qy      800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAG 859
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      892 CTCAGCCCCGGGGGTCCGGACAGCAGAGCAAGGCTCGGATTAGCGCTGTTGCTGCTGAGA 951
Qy      860 TGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      952 TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGTACTTCTGGTCT 1011
Qy      920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCCTCAATGTCTTAAGAGGGTGTTCTGGGATGT 979
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1012 TTGCAATTTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1071
Qy      980 TCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1072 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGTTTCACTTTTTCTCATTTGGCTTG 1131
Qy      1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTCCTCAGTGGCAAATTCCGGG 1099
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1132 TATATGCCAACAGTGCTGCAAACCAATTATTTATAATTTTCTTAGTGGAATTTTCGAG 1191
Qy      1100 AGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGA 1159
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1192 AGGAATTTAAAGCTGCCTTTTCTTGTGTCTTGGGGTTCATCATCGCCAAGGAGACCGCC 1251
Qy      1160 AGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCAAGAGCCGATGCT 1219
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1252 TCGCCAGGGGACGCACGAGCACAGAGAGCAGGAAGTCCCTGACCACACAGATCAGCAACT 1311
Qy      1220 -----CCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGC 1270
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1312 TTGACAATGTATCAAACTCTCAGAGCACGTGGTGCTCACCAGCATAAGCACACTCC 1368

```

# RESULT 8

AK038551

LOCUS AK038551 3729 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230036M08 product:OREXIN RECEPTOR TYPE 2, full insert sequence.

ACCESSION AK038551

VERSION AK038551.1 GI:26332642

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159

REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861

REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3729)  
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome



[illegible]



```

      ||  ||  |   ||| ||  ||||| ||  ||  ||||  ||  ||  ||||| ||
Db      1073 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACCTTTTCTCATTTGGCTTG 1132

Qy      1040 TGTACGCCAACACGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGGCAAATTCCGGG 1099
      |  ||  ||||| ||||| ||||| ||  ||  ||  ||  ||  ||  ||||| ||||| ||  |
Db      1133 TATATGCCAACAGTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGGAAAAATTCGAG 1192

Qy      1100 AGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGA 1159
      ||  |  ||||| ||||| ||  ||  ||  ||  |  |  ||  |  ||  |
Db      1193 AGGAATTTAAAGCTGCCTTTTCTTGTTGTCTTGGGGTTCATCATCGCCAAGGAGACCGCC 1252

Qy      1160 AGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCCAGAGCCGATGCT 1219
      |||  |  |  |  |  |  |||  ||||| ||  ||  ||||  |  |  ||
Db      1253 TCGCCAGGGGACGCACGAGCACAGAGAGCAGGAAGTCCCTGACCACACAGATCAGCAACT 1312

Qy      1220 -----CCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGC 1270
      ||  ||  |||  ||||  ||||| ||||| ||||| ||||| ||  |  ||||  |  |
Db      1313 TTGACAATGTATCAAAACTCTCAGAGCACGTGGTGCTCACCAGCATAAGCACACTCC 1369

```

# RESULT 9

AY420887

LOCUS AY420887 726 bp DNA linear GSS 17-DEC-2003

DEFINITION Mus musculus HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY420887

VERSION AY420887.1 GI:39776844

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 726)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 726)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

```

    source      1..726
                  /organism="Mus musculus"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:10090"
    gene        <1..>726

```

/gene="HCRTR1"  
/locus\_tag="HCM7373"

ORIGIN

Query Match 45.0%; Score 575.4; DB 29; Length 726;  
Best Local Similarity 87.0%; Pred. No. 8e-105;  
Matches 655; Conservative 0; Mismatches 71; Indels 27; Gaps 1;

```
Qy      526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
      |||
Db      1  ATGGTGCCCCAGGCTGCTGTTCATGGAGTGCAGCAGCGTGTGCTGCCTGAGCTAGCCAATCGC 60

Qy      586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
      ||
Db      61 ACCCGGCTCTTCTCTGTCTGTGATGAGCACTGGGCAGATGAACTCTACCCAAGATCTAT 120

Qy      646 CACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
      |||
Db      121 CACAGCTGCTTTTTCATTGTACCTACCTGGCCCCACTGGGCCTCATGGCTATGGCCTAT 180

Qy      706 TTCCAGATATTCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
      |||
Db      181 TTCCAGATCTTCGCAAGCTCTGGGGCCGCCAGATCCCTGGTACCACATCAGCCTTGGTG 240

Qy      766 CGGAACTGGAAGCGCCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
      |||
Db      241 CGGAACTGGAACGGCCCTCGGAACAACCTGGAGGCTCAGCACCAGGGCCTCTGTACAGAG 300

Qy      826 CCCCAGCCCCGGGCCCCGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAG 885
      |||
Db      301 CCCCAGCCCCGGGCCCCGAGCCTTCTGGCTGAGGTGAAGCAGATGCGAGCTCGGAGGAAG 360

Qy      886 ACAGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945
      ||
Db      361 ACGGCTAAGATGCTGATGGTAGTCCTGCTGGTTTTTGCACCTCTGTTATCTGCCATCAGT 420

Qy      946 GTCCTCAATGTCTTAAGAGGGGTGTTCCGGATGTTCCGCCAAGCCAGTGACCGGAAGCT 1005
      |||
Db      421 GTCCTCAATGTCTTAAGAGAGTGTTCCGGATGTTCCGCCAAGCCAGCGACCGGAAGCC 480

Qy      1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
      |||
Db      481 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTAGTGTACGCCAACAGTGCCGCCAACCCCT 540

Qy      1066 ATCATCTACAACCTTCCTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 1125
      |||
Db      541 ATCATCTACAACCTTCCTCAGTGGCAAATTCGGGAGCAGTTCAAGGCTGCCTTCTCCTGC 600

Qy      1126 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCC 1185
      |||
Db      601 TGCCTGCCTGGTCTGG-----GTCCCGGCTCCTCTGCC 633

Qy      1186 AGCCACAAGTCCTTGTCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTG 1245
      ||
Db      634 AGACACAAGTCCTTGTCTTGCAGAGCCGCTGCTCCGTCTCCAAGGTCTCTGAGCATGTC 693

Qy      1246 GTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 1278
```

||||| |||| | ||||| || ||||| |||||  
Db 694 GTGCTGACCACCGTCACTACCGTGCTGTCCTGA 726

RESULT 10

AK079572

LOCUS AK079572 3153 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230091E19 product:OREXIN RECEPTOR TYPE 2, full insert sequence.

ACCESSION AK079572

VERSION AK079572.1 GI:26348079

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source

1. .3153  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM\_DB:A230091E19"  
/db\_xref="MGI:2403517"  
/db\_xref="taxon:10090"  
/clone="A230091E19"  
/sex="male"  
/tissue\_type="hypothalamus"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="adult"

CDS

108. .1202  
/note="unnamed protein product; OREXIN RECEPTOR TYPE 2 (SWISSPROT|P56719, evidence: FASTY, 98.5%ID, 100%length, match=1380)  
putative"  
/codon\_start=1  
/protein\_id="BAC37688.1"  
/db\_xref="GI:26348080"  
/translation="MSSTKLEDSLRRNWSSASELNETQEPFLNPTDYDDEEFLRYLW REYLHPKEYEWVLIAGYIIIVFVALIGNVLVCVAVWKNHHMRTVTNYFIVNLSLADVL VTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVLTLSIALDRWYAICHPL MFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSLPLGLANKTTTFTVCDEHWGGEV YPKMYHICFFLVTYMAPLFLMILAYLQIFRKLWCRQIPGTSSVVQRKWKQQQPVSQPR GSGQQSKARVSAVAEIKQIRARRKTARMLMVVLLVFAICYLPISILNVLKRVFGMFT HTEDRETVYAWFTFPHWLVYANSCCKPNYL"

ORIGIN

Query Match 44.4%; Score 567.6; DB 11; Length 3153;  
Best Local Similarity 68.9%; Pred. No. 5.7e-103;  
Matches 826; Conservative 0; Mismatches 359; Indels 13; Gaps 3;

```
Qy      80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     211 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGAATACCTACACCCGAAAGAATATGAGT 270

Qy     140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCCCTGGTGGGCAACACGCTGG 199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     271 GGGTCCTGATCGCAGGTATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG 330

Qy     200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     331 TCTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACAGTCACCAACTACTTCATAGTCA 390

Qy     260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     391 ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG 450

Qy     320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     451 ACATCACTGAGACTTGGTTCCTTTGGACAGTCCCTCTGTAAGGTCATTTCCTTATTTACAGA 510

Qy     380 CTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     511 CTGTGTGAGTGTCTGTGCTGTTCTTACGTTGAGCTGCATTGCCTTGGACCGATGGTACG 570

Qy     440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGGCGGGCCCGTGGCTCCATCCTGG 499
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     571 CCATTTGTACCCCTTTGATGTTCAAGAGCACAGCCAAACGGGCTCGAAACAGCATCGTTG 630

Qy     500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     631 TCATCTGGATCGTCTCCTGCATCATAATGATTCTCAAGCCATTGTCATGGAGTGCAGCA 690

Qy     560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     691 GCATGCTCCCTGGCCTAGCCAATAAGACCACCCCTCTTTACAGTATGTGATGAACACTGGG 750

Qy     620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     751 GCGGTGAAGTTTACCCAAAGATGTACCATATCTGCTTCTTTCTGGTGACATACATGGCAC 810

Qy     680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     811 CTCTGTTTCTTATGATATTGGCTTATCTCCAAATATTCCGTAAACTCTGGTGCCGACAGA 870

Qy     740 TCCCCGGCACACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCCTCAGACCAGCTGGGGG 799
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     871 TTCCCGGAACCTTCTTCTGTGGTTCAGAGAAAATGGAAGCAGC-----AGCAGCCGTTT 924

Qy     800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCCGCGCCTTCTGGCTGAAG 859
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     925 CTCAGCCCCGGGGGTCCGGACAGCAGAGCAAGGCTCGGGTTAGCGCTGTTGCTGCTGAGA 984

Qy     860 TGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
```

Db 985. TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGTACTTCTGGTCT 1044  
 Qy 920 TCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979  
 Db 1045 TTGCAATTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1104  
 Qy 980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039  
 Db 1105 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACCTTTCCTCATTGGCTTG 1164  
 Qy 1040 TGTACGCCAACAGC-GCTGCCAACCCCATCATCTACAACCTCCTCAGTGGCAAATTCGGG 1098  
 Db 1165 TATATGCCAACAGCTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGGAATAATTCGA 1224  
 Qy 1099 GAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTG 1158  
 Db 1225 GAGGAATTTAAAGCTGCCTTTTCTTGTGTCTTGGGGTTCATCATCGCCAAGGAGACCGC 1284  
 Qy 1159 AAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCTTGCAGAGCCGATGC 1218  
 Db 1285 CTCGCCAGGGGACGCACGAGCACAGAGAGCAGGAAGTCCTGACCACACAGATCAGCAAC 1344  
 Qy 1219 T-----CCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGC 1270  
 Db 1345 TTTGACAATGTATCAAAACTCTCAGAGCACGTGGTGCTCACCAGCATAAGCACACTCC 1402

# RESULT 11

BC035858

LOCUS BC035858 1790 bp mRNA linear HTC 04-MAR-2003

DEFINITION Homo sapiens, Similar to hypocretin (orexin) receptor 2, clone IMAGE:5767576, mRNA.

ACCESSION BC035858

VERSION BC035858.1 GI:23959160

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1790)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc\_mgc@nhgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 79 Row: p Column: 14

This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 6006037

This clone has the following problem: retained intron.

FEATURES	Location/Qualifiers
source	1. .1790
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:5767576"
	/tissue_type="Brain, fetal, whole pooled"
	/clone_lib="NIH_MGC_121"
	/lab_host="DH10B"
	/note="Vector: pCMV-SPORT6"

#### ORIGIN

Query Match 40.8%; Score 521; DB 11; Length 1790;  
Best Local Similarity 70.3%; Pred. No. 9.5e-94;  
Matches 714; Conservative 0; Mismatches 295; Indels 6; Gaps 1;

Qy	80	ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT	139
Db	146	ACGACGAGGAATTCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT	205
Qy	140	GGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCCCTGGTGGGCAACACGCTGG	199
Db	206	GGGTCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG	265
Qy	200	TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	266	TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA	325
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG	319
Db	326	ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG	385
Qy	320	ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG	379
Db	386	ATATCACTGAGACCTGGTTTTTTTGGACAGTCCCTTTGCAAAGTGATTCTTATCTACAGA	445
Qy	380	CTGTGTCCGTGTCTAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG	439
Db	446	CCGTGTCCGTGTCTGTGCTGTCTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG	505
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGGGGCCCGTGGCTCCATCCTGG	499





AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12799331.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 151.r For  
 more information about this cluster, see  
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r)  
[cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r). Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DF013BC02QP1.

FEATURES Location/Qualifiers  
 source 1. .1001  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DF013YE04"  
 /tissue\_type="FETAL BRAIN"  
 /dev\_stage="fetal"  
 /clone\_lib="Homo sapiens FETAL BRAIN"  
 /note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

#### ORIGIN

Query Match 36.8%; Score 470.4; DB 9; Length 1001;  
 Best Local Similarity 91.9%; Pred. No. 1e-83;  
 Matches 543; Conservative 13; Mismatches 26; Indels 9; Gaps 6;

```

Qy      377 AGGCTGTGTCCGTGTTCAGTGGCAGTGCCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 436
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      415 AGGCTGTGTCCGTGTTCANTGGCAGTGCCTAACTCTMANCTTCATCGCMCTGGACCGCTGGT 474

Qy      437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      475 ATGCHATCTGCTACCCACTATTGTTCAAGARACAGCCCGGCGGGCCCGTGGCTCCATCC 534

Qy      497 TGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 556
          | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db      535 TNNGNATCTGGGCTNTNTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 594

Qy      557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 616
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      595 GCAGTGTGCTGCCTNAGCTANCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 654

Qy      617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGG 676
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      655 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGG 714

Qy      677 CCCCCTGGGCTCATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCC 736

```

```

|||||
Db      715 CCCCCTGGGCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 774
Qy      737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGCTGGAAGCGCCCTCAGACCAGCT-G 795
|||||
Db      775 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGCTGGAAGCGCCCTCAGACCAGCTGG 834
Qy      796 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCCGCGCCTTCCTGGCT 855
|||||
Db      835 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCC--AGCCCCGGGCCCCGCGCCTTCCTGGCT 892
Qy      856 GAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGGTGGTGGTGG 915
||||| : | | | | | : | | | | | : | | | | | : | | | | |
Db      893 GAAGTGA---RCAGATGSTGCAGGCAGVAGACASCSAAGATGCTGATGGTGGTGGTGGTGGTGG 949
Qy      916 GTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCTTAAAGAGG 966
: | | | | | : | | | | | : | | | | | : | | | | |
Db      950 STCTTCG-CCTCTGCTACSTG-CCATCAGSGT-CTCAATGTCTTAAAGAGG 997

```

RESULT 13

BQ269289

LOCUS BQ269289 520 bp mRNA linear EST 15-JUL-2003

DEFINITION ik23f12.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5782030 5' similar to SW:OX1R\_HUMAN O43613 OREXIN RECEPTOR TYPE 1 ;, mRNA sequence.

ACCESSION BQ269289

VERSION BQ269289.1 GI:20494355

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 520)

AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu  
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 426.

FEATURES Location/Qualifiers



BX409735  
LOCUS BX409735 892 bp mRNA linear EST 13-MAY-2003  
DEFINITION BX409735 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
CS0DF013YE04 5-PRIME, mRNA sequence.

ACCESSION BX409735

VERSION BX409735.1 GI:30652997

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 892)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 151.r For  
more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0BAF012ZE07\\_AF01110\\_1&cluster=151.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAF012ZE07_AF01110_1&cluster=151.r)

Contact : Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0BAF012ZE07\_AF01110\_1.

FEATURES

source

Location/Qualifiers

1..892

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DF013YE04"

/tissue\_type="FETAL BRAIN"

/dev\_stage="fetal"

/clone\_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

ORIGIN

Query Match 34.2%; Score 437.4; DB 13; Length 892;

Best Local Similarity 99.8%; Pred. No. 3.9e-77;

Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 840 CCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCT 899

|||||

Db 1 CCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCT 60

Qy 900 GATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCT 959

|||||

Db 61 GATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCT 120

Qy 960 TAAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTT 1019

|||||

Db 121 TAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTT 180

Qy 1020 CACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1079  
 |||

Db 181 CACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 240

Qy 1080 CCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCT 1139  
 |||

Db 241 CCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCT 300

Qy 1140 GGGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTT 1199  
 |||

Db 301 GGGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTT 360

Qy 1200 GTCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGT 1259  
 |||

Db 361 GTCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGT 420

Qy 1260 CACCACAGTGCTGCCCTGA 1278  
 |||

Db 421 CACCACAGTGCTGCCCTGA 439

# RESULT 15

BM926746

LOCUS BM926746 993 bp mRNA linear EST 12-MAR-2002  
 DEFINITION AGENCOURT\_6681991 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5767576  
 5', mRNA sequence.

ACCESSION BM926746

VERSION BM926746.1 GI:19377125

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 993)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999).

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12826 row: a column: 17

High quality sequence stop: 684.

## FEATURES

source

Location/Qualifiers

1. .993

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5767576"

/lab\_host="DH10B"

```

/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

```

ORIGIN

```

Query Match          30.8%; Score 393.2; DB 12; Length 993;
Best Local Similarity 72.1%; Pred. No. 2.9e-68;
Matches 512; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

```

```

Qy      80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     145 ACGACGAGGAATTCTCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 204

Qy     140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCCCTGGTGGGCAACACGCTGG 199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     205 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTGTCGTGGCTCTCATTGGGAACGTCCTGG 264

Qy     200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     265 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 324

Qy     260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     325 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 384

Qy     320 ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCATCTACAGG 379
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     385 ATATCACTGAGACCTGGTTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCCTTATCTACAGA 444

Qy     380 CTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     445 CCGTGTCCGTGTCTGTGTCTGTCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 504

Qy     440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGCGGGCCCGTGGCTCCATCCTGG 499
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     505 CAATCTGTACCCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATGTCA 564

Qy     500 GCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     565 TCATCTGGATTGTCTCTCTGCATTATAATGATTCTCAGGCCATCGTCATGGAGTGCAGCA 624

Qy     560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     625 CCGTGTTCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 684

Qy     620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC 679
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     685 GTGGTGAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 744

```

Search completed: October 15, 2004, 22:50:27  
Job time : 3725.85 secs

Search completed: October 15, 2004, 22:50:27  
Job time : 3725.85 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:54:41 ; Search time 5178.06 Seconds  
(without alignments)  
10697.520 Million cell updates/sec

Title: US-10-070-532-1  
Perfect score: 1278  
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgcctgccctga 1278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*



28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	1274.8	99.7	1564	6	E43974	E43974 Novel G pro
2	1274.8	99.7	1564	6	E50810	E50810 Novel G pro
3	1274.8	99.7	1564	6	E50811	E50811 Novel G pro
4	1274.8	99.7	1564	6	AX299473	AX299473 Sequence
5	1274.8	99.7	1564	6	AX299475	AX299475 Sequence
6	1274.8	99.7	1564	6	AX549082	AX549082 Sequence
7	1274.8	99.7	1564	6	AX746121	AX746121 Sequence
8	1274.8	99.7	1564	6	AX840912	AX840912 Sequence
9	1274.8	99.7	1564	9	AF041243	AF041243 Homo sapi
10	1270	99.4	1278	6	AX280925	AX280925 Sequence
11	1205.8	94.4	1209	6	AR216117	AR216117 Sequence
12	1201	94.0	1209	6	BD185452	BD185452 Human neu
13	1086.4	85.0	1133	6	E43973	E43973 Novel G pro
14	1086.4	85.0	1133	6	AX746120	AX746120 Sequence
15	1086.4	85.0	1170	6	E43972	E43972 Novel G pro
16	1086.4	85.0	1170	6	AX746118	AX746118 Sequence
17	1085.8	85.0	1110	6	AR216118	AR216118 Sequence
18	1083.2	84.8	1116	6	AR216119	AR216119 Sequence
19	1083.2	84.8	1133	6	BD185454	BD185454 Human neu
20	1077.8	84.3	1110	6	BD185453	BD185453 Human neu
21	998	78.1	2200	10	AY336083	AY336083 Mus muscu
22	991.6	77.6	2469	10	AF041244	AF041244 Rattus no
23	699.2	54.7	843	6	AR109899	AR109899 Sequence
24	672.2	52.6	789	6	AR109632	AR109632 Sequence
25	672.2	52.6	789	6	E12154	E12154 cDNA encodi
26	672.2	52.6	789	6	AR300942	AR300942 Sequence
27	640.2	50.1	781	10	AF394596	AF394596 Mus muscu
28	601.2	47.0	3114	10	AF041246	AF041246 Rattus no
29	578.6	45.3	1545	10	AY336084	AY336084 Mus muscu
30	578.6	45.3	2117	10	AY336085	AY336085 Mus muscu
31	554.4	43.4	1633	6	E33974	E33974 cDNA clone
32	554.4	43.4	1843	6	AX549084	AX549084 Sequence
33	554.4	43.4	1843	6	AX840914	AX840914 Sequence

34	554.4	43.4	1878	9	AF041245	AF041245 Homo sapi
35	549.6	43.0	1335	6	AX280927	AX280927 Sequence
36	541.6	42.4	1805	4	AF164626	AF164626 Canis fam
37	497.8	39.0	597	10	AY255599	AY255599 Mus muscu
38	330.8	25.9	382	4	AF499612	AF499612 Ovis arie
39	304.2	23.8	637	10	AF394597	AF394597 Mus muscu
40	281.6	22.0	328	4	AB092488	AB092488 Bos tauru
41	263.2	20.6	501	4	AF532967	AF532967 Ovis arie
42	249.2	19.5	344	9	F202078S03	AF202080 Homo sapi
43	249.2	19.5	9785	6	AR178605	AR178605 Sequence
44	249.2	19.5	9785	6	AX088174	AX088174 Sequence
45	249.2	19.5	9785	9	AY062030	AY062030 Homo sapi

# ALIGNMENTS

## RESULT 1

E43974

LOCUS E43974 1564 bp DNA linear PAT 31-JAN-2002

DEFINITION Novel G protein-coupled receptor (HFGAN72Y).

ACCESSION E43974

VERSION E43974.1 GI:18625173

KEYWORDS JP 2000106888-A/3.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1564)

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE Novel G protein-coupled receptor (HFGAN72Y)

JOURNAL Patent: JP 2000106888-A 3 18-APR-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000106888-A/3

PD 18-APR-2000

PF 21-JUL-1999 JP 1999206116

PR 30-APR-1997 US 08/846705

PI DERK J BERGSMA,CATHARINE ELIZABETH ELLIS

PC C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC A61P1/14,

PC A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC A61P13/08,

PC A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,

PC A61P31/04,

PC A61P31/10,A61P31/12,A61P31/18,A61P33/00,A61P35/00,A61P37/08,

PC A61P43/00,

PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,

PC G01N33/577//

PC C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,

PC A61K37/02,

PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91)

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1. .1564

FT /organism='Unidentified'.

FEATURES

Location/Qualifiers

source 1. .1564  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;  
Best Local Similarity 99.8%; Pred. No. 9.4e-244;  
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
      |||
Db     154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      |||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
      |||
Db     274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
      |||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
      |||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
      |||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
      |||
Db     514 GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
      |||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
      |||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
      |||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
      |||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
      |||
Db     814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873
```

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 Qy 1081 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1234 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353  
 Qy 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1354 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413  
 Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 ||||||||||||||||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431

# RESULT 2

E50810

LOCUS E50810 1564 bp DNA linear PAT 18-JUN-2001

DEFINITION Novel G protein-bound receptor (HFGAN 72X).

ACCESSION E50810

VERSION E50810.1 GI:13023197

KEYWORDS JP 2000060578-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1564)

AUTHORS Derk, J.B. and Catharine, E.E.

TITLE Novel G protein-bound receptor (HFGAN 72X)

JOURNAL Patent: JP 2000060578-A 1 29-FEB-2000;

SMITHKLINE BEECHAM CORP



Db	514	GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGTCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGTCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1233
Qy	1081	CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1234	CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1293
Qy	1141	GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1294	GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1353
Qy	1201	TCCTTGCAAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1260
Db	1354	TCCTTGCAAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1413

Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431

# RESULT 3

E50811

LOCUS E50811 1564 bp DNA linear PAT 18-JUN-2001

DEFINITION Novel G protein-bound receptor (HFGAN 72X).

ACCESSION E50811

VERSION E50811.1 GI:13023198

KEYWORDS JP 2000060578-A/2.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1564)

AUTHORS Derk, J.B. and Catharine, E.E.

TITLE Novel G protein-bound receptor (HFGAN 72X)

JOURNAL Patent: JP 2000060578-A 2 29-FEB-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000060578-A/2

PD 29-FEB-2000

PF 21-JUL-1999 JP 1999206115

PR 30-APR-1997 US 08/846704

PI DERK J BERGSMA, CATHARINE ELIZABETH ELLIS

PC C12N15/09, A61K31/70, A61K38/00, A61K39/00, A61K39/395, A61K39/395,

PC A61K45/00,

PC A61K48/00, A61P3/04, A61P9/00, A61P11/06, A61P13/00, A61P25/00, PC  
 A61P25/16,

PC A61P25/18, A61P25/20, A61P25/22, A61P31/04, A61P31/10, A61P31/12,

PC A61P31/18,

PC A61P35/00, A61P37/00, C07K14/705, C12N5/10, C12P21/02, C12Q1/02, PC  
 G01N33/53,

PC G01N33/566//C07K16/28, C12N15/00, A61K37/02, C12N5/00 CC

Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1. .1564

FT /organism='Unidentified'.

FEATURES Location/Qualifiers

source 1. .1564

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

## ORIGIN

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;

Best Local Similarity 99.8%; Pred. No. 9.4e-244;

Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

|||||

Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Db	214	 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	274	 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	874	 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934	 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960



Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||

Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||

Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233

Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||

Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||

Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||

Db 1354 TCCTTGAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||

Db 1414 ACCACAGTGCTGCCCTGA 1431

#### RESULT 4

AX299473

LOCUS AX299473 1564 bp DNA linear PAT 26-NOV-2001

DEFINITION Sequence 1 from Patent EP1154019.

ACCESSION AX299473

VERSION AX299473.1 GI:17129230

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Bergsma, D.J. and Ellis, C.E.

TITLE G-protein coupled receptor (hfgan72x)

JOURNAL Patent: EP 1154019-A 1 14-NOV-2001;  
 SmithKline Beecham Corporation (US)

FEATURES

Location/Qualifiers  
 source 1. .1564  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 9.4e-244;  
 Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60  
 |||

Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	1053

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCCATCAGCGTCCTCAATGTCCTT 1113

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 |||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1233

Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy 1201 TCCTTGCAAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||  
 Db 1354 TCCTTGCAAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431

RESULT 5  
 AX299475

LOCUS AX299475 1564 bp DNA linear PAT 26-NOV-2001

DEFINITION Sequence 3 from Patent EP1154019.

ACCESSION AX299475

VERSION AX299475.1 GI:17129231

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE G-protein coupled receptor (hfgan72x)

JOURNAL Patent: EP 1154019-A 3 14-NOV-2001;  
 SmithKline Beecham Corporation (US)

FEATURES

source

Location/Qualifiers

1. .1564

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;

Best Local Similarity 99.8%; Pred. No. 9.4e-244;

Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Db	154		ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61		TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214		TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121		TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	274		TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	333
Qy	181		CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334		CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241		ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394		ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301		CCGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454		CCGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661		ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814		ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	874		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	933
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	993
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900

```

Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113
Qy      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173
Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233
Qy     1081 CTCAGTGGCAAATTCGGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1234 CTCAGTGGCAAATTCGGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293
Qy     1141 GGTCCTGCGGCTCTCTGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1294 GGTCCTGCGGCTCTCTGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353
Qy     1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
        |||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     1354 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413
Qy     1261 ACCACAGTGCTGCCCTGA 1278
        ||||||||||||||||||
Db     1414 ACCACAGTGCTGCCCTGA 1431

```

# RESULT 6

AX549082

LOCUS AX549082 1564 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 367 from Patent WO02061087.

ACCESSION AX549082

VERSION AX549082.1 GI:25813851

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors  
(GPCRs), antibodies thereto, and systems for identifying such  
antigenic peptides

JOURNAL Patent: WO 02061087-A 367 08-AUG-2002;

Lifespan Biosciences, Inc. (US)

FEATURES

source

Location/Qualifiers

1..1564

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match

99.7%; Score 1274.8; DB 6; Length 1564;

Best Local Similarity 99.8%; Pred. No. 9.4e-244;  
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        |||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        |||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC 180
        |||
Db     274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        |||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        |||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC 420
        |||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        |||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGTGGCCATCATGGTGCCCCAGGCT 540
        |||
Db     634 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        |||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        |||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTACCTACCTGGCCCCACTGGGCCATGGCCATGGCCTATTTCCAGATATTCCGC 720
        |||
Db     814 ATTGTACCTACCTGGCCCCACTGGGCCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780
        |||
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
        |||
```

Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||

Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy 901 ATGGTGGTGTCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||

Db 1054 ATGGTGGTGTCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||

Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080  
 |||

Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1233

Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||

Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||

Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy 1201 TCCTTGCAAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGTCTACCAGCGTC 1260  
 |||

Db 1354 TCCTTGCAAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGTCTACCAGCGTC 1413

Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||

Db 1414 ACCACAGTGCTGCCCTGA 1431

# RESULT 7

AX746121

LOCUS AX746121 1564 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 4 from Patent EP1156110.

ACCESSION AX746121

VERSION AX746121.1 GI:31744927

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE G-protein coupled receptor (HFGAN72Y)

JOURNAL Patent: EP 1156110-A 4 21-NOV-2001;

SMITHKLINE BEECHAM CORPORATION (US)

FEATURES Location/Qualifiers

source 1..1564

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/note="HGS EST 554692"

ORIGIN

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 9.4e-244;  
 Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCCTGGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCCTGGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	933



Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993  
 |||  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 |||  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 |||  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 1114 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 |||  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 |||  
 Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 |||  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353  
 |||  
 Qy 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||  
 Db 1354 TCCTTGAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413  
 |||  
 Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431  
 |||

# RESULT 8

AX840912

LOCUS AX840912 1564 bp DNA linear PAT 16-DEC-2003

DEFINITION Sequence 8 from Patent WO03075945.

ACCESSION AX840912

VERSION AX840912.1 GI:39979051

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Eulenberg,K., Steuernagel,A., Haeder,T. and Broenner,G.

TITLE Cg8327, cg10823, cg18418, cg15862, cg3768, cg11447 and cg16750  
 homologous proteins involved in the regulation of energy  
 homeostasis

JOURNAL Patent: WO 03075945-A 8 18-SEP-2003;

DeveloGen Aktiengesellschaft fuer entwicklungsbiologische;  
 Forschung (DE)

```

FEATURES                      Location/Qualifiers
  source                      1. .1564
                              /organism="Homo sapiens"
                              /mol_type="unassigned DNA"
                              /db_xref="taxon:9606"

```

ORIGIN

```

Query Match          99.7%;  Score 1274.8;  DB 6;  Length 1564;
Best Local Similarity 99.8%;  Pred. No. 9.4e-244;
Matches 1276;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

```

```

Qy      1  ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61  TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661  ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db 814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 |||

Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||

Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900  
 |||

Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 1053

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||

Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC 1020  
 |||

Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGTGCCAACCCCATCATCTACAACCTTC 1080  
 |||

Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGTGCCAACCCCATCATCTACAACCTTC 1233

Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||

Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCCTTG 1200  
 |||

Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCCTTG 1353

Qy 1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTACCAGCGTC 1260  
 |||

Db 1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTACCAGCGTC 1413

Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||

Db 1414 ACCACAGTGCTGCCCTGA 1431

# RESULT 9

AF041243

LOCUS AF041243 1564 bp mRNA linear PRI 24-FEB-1998

DEFINITION Homo sapiens orexin receptor-1 mRNA, complete cds.

ACCESSION AF041243

VERSION AF041243.1 GI:2897123

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1564)

AUTHORS Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M.,  
 Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P.,

Wilson, S., Arch, J.R.S., Buckingham, R.E., Haynes, A.C., A. Carr, S.A.,  
 Annan, R.S., McNulty, D.E., Liu, W.-S., Terrett, J.A.,  
 Elshourbagy, N.A., Bergsma, D.J. and Yanagisawa, M.

TITLE Orexins and orexin receptors: a family of hypothalamic  
 neuropeptides and G protein-coupled receptors that regulate feeding  
 behavior

JOURNAL Cell 92 (4), 573-585 (1998)

MEDLINE 98150861

PUBMED 9491897

REFERENCE 2 (bases 1 to 1564)

AUTHORS Sakurai, T., Amemiya, A., Ishii, M., Matsuzaki, I., Chemelli, R.M.,  
 Tanaka, H., Williams, S.C., Richardson, J.A., Kozlowski, G.P.,  
 Wilson, S., Arch, J.R.S., Buckingham, R.E., Haynes, A.C., A. Carr, S.A.,  
 Annan, R.S., McNulty, D.E., Liu, W.-S., Terrett, J.A.,  
 Elshourbagy, N.A., Bergsma, D.J. and Yanagisawa, M.

TITLE Direct Submission

JOURNAL Submitted (07-JAN-1998) HHMI/Department of Molecular Genetics,  
 University of Texas Southwestern Medical Center at Dallas, 5323  
 Harry Hines Blvd., Rm. Y5.224, Dallas, TX 75235-9050, USA

FEATURES Location/Qualifiers

source 1. .1564  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /chromosome="1"  
 /map="1p33"

CDS 154. .1431  
 /note="OX1R; G protein-coupled receptor"  
 /codon\_start=1  
 /product="orexin receptor-1"  
 /protein\_id="AAC39601.1"  
 /db\_xref="GI:2897124"  
 /translation="MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLYPKQ  
 YEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPA  
 SLLVDITESWLFHALCKVIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARR  
 ARGSI LGIWA VSLA IMVPQA AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSC  
 FFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEP  
 QPRGRAFLAEVKQMRARRKTAKMLMVVLLVFALCYLPISVLNVLKR VFGMFRQASDRE  
 AVYACFTTFSHWLVYANSAANPIIYNFLSGKFREQFAAFSCCLPGLGPCGSLKAPSPR  
 SSASHKSLSLSQSRCSISKISEHVVLTSVTTVLP"

# ORIGIN

Query Match 99.7%; Score 1274.8; DB 9; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 9.4e-244;  
 Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGGCC 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGGCC 333
  
```

Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 |||  
 Db 334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 |||  
 Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 |||  
 Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||  
 Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||  
 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 |||  
 Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||  
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 |||  
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 993

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233

Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy 1201 TCCTTGCAAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||  
 Db 1354 TCCTTGCAAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431

# RESULT 10

AX280925

LOCUS AX280925 1278 bp DNA linear PAT 02-NOV-2001

DEFINITION Sequence 548 from Patent WO0177172.

ACCESSION AX280925

VERSION AX280925.1 GI:16608218

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.

TITLE Non-endogenous, constitutively activated known G protein-coupled  
 receptors

JOURNAL Patent: WO 0177172-A 548 18-OCT-2001;  
 Arena Pharmaceuticals, Inc. (US)

FEATURES

Location/Qualifiers

source

1. 1278

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 99.4%; Score 1270; DB 6; Length 1278;

Best Local Similarity 99.6%; Pred. No. 8.7e-243;

Matches 1273; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

|||||

Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

|||||

Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180  
 |||  
 Db 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180

Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 |||  
 Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 |||  
 Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 |||  
 Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||  
 Db 361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||  
 Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 |||  
 Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||  
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 |||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

```

Db      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
Qy      1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
Db      1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
Qy      1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
Db      1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
Qy      1201 TCCTTGCAAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
Db      1201 TCCTTGCAAGAGCCGATGCTCCATCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
Qy      1261 ACCACAGTGCTGCCCTGA 1278
Db      1261 ACCACAGTGCTGCCCTGA 1278

```

# RESULT 11

AR216117

LOCUS AR216117 1209 bp DNA linear PAT 25-SEP-2002

DEFINITION Sequence 1 from patent US 6410701.

ACCESSION AR216117

VERSION AR216117.1 GI:23314430

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1209)

AUTHORS Soppet,D.R., Li,Y. and Rosen,C.A.

TITLE Human neuropeptide receptor

JOURNAL Patent: US 6410701-A 1 25-JUN-2002;

FEATURES Location/Qualifiers

source 1..1209

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Query Match 94.4%; Score 1205.8; DB 6; Length 1209;

Best Local Similarity 99.8%; Pred. No. 5.4e-230;

Matches 1207; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
Db      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
Qy      121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

```



Db	121	 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	 GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	 GCCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721	 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781	 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	 ATGGTGGTGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020

```

Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
Qy      1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
Qy      1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
Qy      1201 TCCTTGCA 1209
        |||||
Db      1201 TCCTTGTA 1209

```

RESULT 12

BD185452

LOCUS BD185452 1209 bp DNA linear PAT 17-JUN-2003

DEFINITION Human neuropeptide receptor.

ACCESSION BD185452

VERSION BD185452.1 GI:31877652

KEYWORDS JP 2002360288-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1209)

AUTHORS Soppet,D.R., Li,Y. and Rosen,C.A.

TITLE Human neuropeptide receptor

JOURNAL Patent: JP 2002360288-A 1 17-DEC-2002;

HUMAN GENOME SCIENCES INC

COMMENT OS Unidentified

PN JP 2002360288-A/1

PD 17-DEC-2002

PF 02-MAY-2002 JP 2002130838

PI DANIEL R SOPPET,YI LI,CRAIG A ROSEN

PC C12N15/09,A61K31/7088,A61K38/00,A61K45/00,A61K48/00,A61P3/04,

PC A61P3/06,

PC A61P3/10,A61P9/10,A61P9/12,A61P25/08,A61P25/18,A61P25/22, PC

A61P25/28,

PC A61P35/00,A61P43/00,C07K14/705,C07K16/24,C12N1/15,C12N1/19, PC

C12N1/21,

PC C12N5/10,C12Q1/68,C12N15/00,C12N5/00,A61K37/02 CC

Strandedness: Single;

CC Topology: Linear;

CC Human neuropeptide receptor

FH Key Location/Qualifiers

FT source 1. .1209

FT /organism='Unidentified'.

FEATURES Location/Qualifiers

source 1. .1209

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

ORIGIN

Query Match 94.0%; Score 1201; DB 6; Length 1209;  
 Best Local Similarity 99.6%; Pred. No. 4.8e-229;  
 Matches 1204; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721	AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780

Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Qy	1081	CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1081	CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Qy	1141	GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1141	GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Qy	1201	TCCTTGCTAG	1209
Db	1201	TCCTTGCTAG	1209

# RESULT 13

E43973

LOCUS E43973 1133 bp DNA linear PAT 31-JAN-2002

DEFINITION Novel G protein-coupled receptor (HFGAN72Y).

ACCESSION E43973

VERSION E43973.1 GI:18625172

KEYWORDS JP 2000106888-A/2.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1133)

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE Novel G protein-coupled receptor (HFGAN72Y)

JOURNAL Patent: JP 2000106888-A 2 18-APR-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000106888-A/2

PD 18-APR-2000

PF 21-JUL-1999 JP 1999206116

PR 30-APR-1997 US 08/846705

PI DERK J BERGSMA,CATHARINE ELIZABETH ELLIS

PC C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC A61P1/14,

PC A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC  
A61P13/08,  
PC A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,  
PC A61P31/04,  
PC A61P31/10,A61P31/12,A61P31/18,A61P33/00,A61P35/00,A61P37/08,  
PC A61P43/00,  
PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,  
PC G01N33/577//  
PC C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,  
PC A61K37/02,  
PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91)  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1. .1133  
FT /organism='Unidentified'.

FEATURES Location/Qualifiers  
source 1. .1133  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

# ORIGIN

Query Match 85.0%; Score 1086.4; DB 6; Length 1133;  
Best Local Similarity 99.9%; Pred. No. 3.3e-206;  
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	121	TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480

Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGG 1088  
 ||||||||  
 Db 1081 CTCAGTGG 1088

RESULT '14

AX746120

LOCUS AX746120 1133 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 3 from Patent EP1156110.

ACCESSION AX746120

VERSION AX746120.1 GI:31744926

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Bergsma,D.J. and Ellis,C.E.  
TITLE G-protein coupled receptor (HFGAN72Y)  
JOURNAL Patent: EP 1156110-A 3 21-NOV-2001;  
SMITHKLINE BEECHAM CORPORATION (US)

FEATURES Location/Qualifiers  
source 1. .1133  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/note="HGS EST 557082"

# ORIGIN

Query Match 85.0%; Score 1086.4; DB 6; Length 1133;  
Best Local Similarity 99.9%; Pred. No. 3.3e-206;  
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 |||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGTGCCAAACCCCATCATCTACAATTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGTGCCAAACCCCATCATCTACAATTC 1080

Qy 1081 CTCAGTGG 1088  
 |||  
 Db 1081 CTCAGTGG 1088

# RESULT 15

E43972

LOCUS E43972 1170 bp DNA linear PAT 31-JAN-2002

DEFINITION Novel G protein-coupled receptor (HFGAN72Y).

ACCESSION E43972

VERSION E43972.1 GI:18625171

KEYWORDS JP 2000106888-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1170)

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE Novel G protein-coupled receptor (HFGAN72Y)

JOURNAL Patent: JP 2000106888-A 1 18-APR-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000106888-A/1

PD 18-APR-2000

PF 21-JUL-1999 JP 1999206116



PR 30-APR-1997 US 08/846705  
 PI DERK J BERGSMAN, CATHARINE ELIZABETH ELLIS  
 PC C12N15/09, A61K38/00, A61K38/00, A61K45/00, A61K48/00, A61P1/00, PC  
 A61P1/14,  
 PC A61P9/02, A61P9/04, A61P9/10, A61P9/12, A61P11/06, A61P13/02, PC  
 A61P13/08,  
 PC A61P19/10, A61P25/14, A61P25/16, A61P25/18, A61P25/22, A61P25/24,  
 PC A61P31/04,  
 PC A61P31/10, A61P31/12, A61P31/18, A61P33/00, A61P35/00, A61P37/08,  
 PC A61P43/00,  
 PC C07K14/705, C07K16/28, C12N1/21, C12N5/10, C12P21/02, G01N33/566,  
 PC G01N33/577//  
 PC C12P21/08, (C12N15/09, C12R1:91), (C12P21/02, C12R1:91), C12N15/00,  
 PC A61K37/02,  
 PC A61K37/02, C12N5/00, (C12N15/00, C12R1:91)  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1. .1170  
 FT /organism='Unidentified'.

FEATURES Location/Qualifiers  
 source 1. .1170  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

# ORIGIN

Query Match 85.0%; Score 1086.4; DB 6; Length 1170;  
 Best Local Similarity 99.9%; Pred. No. 3.3e-206;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420

Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAC TGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAC TGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC	1080
Qy	1081	CTCAGTGG	1088
Db	1081	CTCAGTGG	1088

Search completed: October 15, 2004, 19:59:34  
 Job time : 5183.06 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:52:46 ; Search time 545.899 Seconds  
(without alignments)  
9945.416 Million cell updates/sec

Title: US-10-070-532-1  
Perfect score: 1278  
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgcctgcctga 1278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1278	100.0	1278	4 AAS00491	Aas00491 Human neu
2	1274.8	99.7	1564	2 AAV63468	Aav63468 cDNA enco
3	1274.8	99.7	1564	2 AAV68514	Aav68514 Nucleotid
4	1274.8	99.7	1564	4 AAS17464	Aas17464 Human G p
5	1274.8	99.7	1564	4 AAF32103	Aaf32103 Human HFG
6	1274.8	99.7	1564	6 ABA96021	Aba96021 HGS EST 5
7	1274.8	99.7	1564	6 AAI64173	Aai64173 HFGAN72X

8	1274.8	99.7	1564	6	AAI64172	Aai64172	Human HFG
9	1274.8	99.7	1564	7	ABZ42789	Abz42789	Human ore
10	1270	99.4	1278	5	ABI98014	Abi98014	Non-endog
11	1225.2	95.9	1278	4	AAD09335	Aad09335	Cynomolgo
12	1202.6	94.1	1209	2	AAT42826	Aat42826	Neuropept
13	1086.4	85.0	1133	2	AAV68512	Aav68512	Nucleotid
14	1086.4	85.0	1133	6	ABA96020	Aba96020	HGS EST 5
15	1086.4	85.0	1170	2	AAV68511	Aav68511	Nucleotid
16	1086.4	85.0	1170	6	ABA96019	Aba96019	G-protein
17	1085.8	85.0	1110	2	AAT42827	Aat42827	Neuropept
18	1084.8	84.9	1133	4	AAS00493	Aas00493	Human neu
19	1083.2	84.8	1133	2	AAT42828	Aat42828	Neuropept
20	1083	84.7	1281	5	AAC85974	Aac85974	Dog orexi
21	1077.8	84.3	1110	4	AAS00492	Aas00492	Human neu
22	672.2	52.6	789	2	AAT13909	Aat13909	Rabbit G-
23	672.2	52.6	789	2	AAT51065	Aat51065	G-protein
24	554.4	43.4	1633	2	AAX29700	Aax29700	Human 7-t
25	554.4	43.4	1843	7	ABZ42790	Abz42790	Human ore
26	549.6	43.0	1335	4	AAF90300	Aaf90300	Nucleotid
27	549.6	43.0	1335	5	ABI98015	Abi98015	Non-endog
28	249.2	19.5	344	5	AAF56748	Aaf56748	Human HCR
29	249.2	19.5	9785	5	AAF55159	Aaf55159	Nucleotid
30	249.2	19.5	10453	4	AAS17462	Aas17462	Human G p
31	244	19.1	244	4	AAS17449	Aas17449	Human G p
32	231.6	18.1	331	5	AAF56750	Aaf56750	Human HCR
33	227	17.8	227	4	AAS17453	Aas17453	Human G p
34	199	15.6	356	4	AAS17445	Aas17445	Human G p
35	198.6	15.5	452	5	AAF56746	Aaf56746	Human HCR
36	191.6	15.0	374	5	AAF56752	Aaf56752	Human HCR
37	189.4	14.8	324	4	AAS17457	Aas17457	Human G p
38	188.8	14.8	1287	2	AAV68513	Aav68513	Nucleotid
39	188.8	14.8	1287	6	ABA96022	Aba96022	Sac I sub
40	181	14.2	263	5	AAF56747	Aaf56747	Human HCR
41	179	14.0	179	4	AAS17447	Aas17447	Human G p
42	163.2	12.8	1290	3	AAA70507	Aaa70507	Novel hum
43	163.2	12.8	1290	3	AAA70508	Aaa70508	Novel hum
44	163.2	12.8	1290	4	AAH78518	Aah78518	Nucleotid
45	163.2	12.8	1290	4	AAH78519	Aah78519	Nucleotid

#### ALIGNMENTS

##### RESULT 1

AAS00491

ID AAS00491 standard; cDNA; 1278 BP.

XX

AC AAS00491;

XX

DT 17-MAY-2001 (first entry)

XX

DE Human neuropeptide receptor cDNA.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;

KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;

KW cardiovascular disorder; autoimmune disorder; infectious disorder;

KW eating behaviour disorder; narcolepsy; neurological disease;



Db	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Qy	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900

QY 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

QY 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

QY 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080

QY 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

QY 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

QY 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||  
 Db 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260

QY 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1261 ACCACAGTGCTGCCCTGA 1278

## RESULT 2

AAV63468

ID AAV63468 standard; cDNA; 1564 BP.

XX

AC AAV63468;

XX

DT 26-JAN-1999 (first entry)

XX

DE cDNA encoding G-protein coupled receptor (HFGAN72X) polypeptide.

XX

KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;

KW bulimia; asthma; Parkinson's disease; acute heart failure;

KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KW benign prostatic hypertrophy; neurological disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 154..1431

FT /\*tag= a

FT /product= "HFGAN72X"

XX

PN EP875566-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308563.





Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513  
 Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573  
 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633  
 Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813  
 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 Qy 1081 CTCAGTGCCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1234 CTCAGTGCCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy 1201 TCCTTGCAGAGCCGATGCTCCGTCCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||  
 Db 1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413  
 Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431

RESULT 3

AAV68514

ID AAV68514 standard; cDNA; 1564 BP.

XX

AC AAV68514;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of a probe HGS EST 554692.

XX

KW Probe HGS EST 554692; G-protein coupled receptor family; HFGAN72Y;

KW mutation; probe; agonist; antagonist; activation; inhibition;

KW gene therapy; antibody; immune response; vaccine; HIV-1; HIV-2; cancer;

KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;

KW hypotension; hypertension; urinary retention; osteoporosis;

KW angina pectoris; myocardial infarction; ulcer; allergies;

KW psychotic disorder; neurological disorder; gene mapping; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX

PR 30-APR-1997; 97US-00846705.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis C;

XX

DR WPI; 1998-570286/49.

XX

PT New G-protein coupled Receptor HFGAN72Y polypeptide and polynucleotide -

PT useful as diagnostic reagents and for prevention and treatment of HIV

PT infections, cancer, osteoporosis and Parkinson's disease.

XX

PS Example 1; Page 19-20; 22pp; English.

XX

CC This is the nucleotide sequence of the probe HGS EST 554692 used in the

CC method of the invention involving the G-protein coupled receptor,

CC HFGAN72Y. Its polypeptides and polynucleotides are useful for diagnosing

CC susceptibility to diseases by detecting mutations in the HFGAN72Y gene

CC using probes containing the HFGAN72Y nucleotide sequence, and can

CC diagnose diseases associated with HFGAN72Y imbalance by determining

CC HFGAN72Y polypeptide or mRNA expression levels. Agonists/antagonists can  
 CC be used in treatment to activate/inhibit HFGAN72Y activity, in addition  
 CC to direct administration of antisense sequences to prevent expression, or  
 CC HFGAN72Y polypeptides to treat conditions associated with a lack HFGAN72Y  
 CC protein. Gene therapy may also be used to affect endogenous HFGAN72Y  
 CC polypeptide production. HFGAN72Y antibodies are useful for inducing an  
 CC immune response to immunise and prevent diseases, and for isolating  
 CC HFGAN72Y clones or purifying the polypeptides by affinity chromatography.  
 CC HFGAN72Y polypeptides can be administered directly or as a vaccine to  
 CC inoculate against diseases. Diseases diagnosed, prevented or treated  
 CC include HIV-1 or HIV-2 infections, pain, cancers, anorexia, bulimia,  
 CC asthma, Parkinson's disease, acute heart failure, hypotension,  
 CC hypertension, urinary retention, osteoporosis, angina pectoris,  
 CC myocardial infarction, ulcers; allergies, benign prostatic hypertrophy,  
 CC and psychotic and neurological disorders. The HFGAN72Y polypeptide is  
 CC also useful for mapping the gene to a chromosome, allowing gene  
 CC inheritance to be studied through linkage analysis

XX

SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 99.7%; Score 1274.8; DB 2; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-288;  
 Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	274	TACCCAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540

Db	634	 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCAGATATTCCGC	720
Db	814	 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	874	 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934	 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1020
Db	1114	 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1080
Db	1174	 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1233
Qy	1081	CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1234	 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1293
Qy	1141	GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1294	 GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1353
Qy	1201	TCCTTGAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1260
Db	1354	 TCCTTGAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1413
Qy	1261	ACCACAGTGCTGCCCTGA	1278
Db	1414	 ACCACAGTGCTGCCCTGA	1431

AAS17464

ID AAS17464 standard; DNA; 1564 BP.

XX

AC AAS17464;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72 variant CDS.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72; ds;

KW bacterial infection; fungal infection; protozoan infection;

KW viral infection; human immunodeficiency virus; HIV; cancer; diabetes;

KW Parkinson's disease; osteoporosis; myocardial infarction; ulcer; asthma;

KW allergy; angina pectoris; renal disease; depression; schizophrenia;

KW anorexia; obesity; Kallman's syndrome; hypothalamic disorder;

KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;

KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 154..1431

FT /\*tag= a

FT /product= "HFGAN71X variant"

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

DR P-PSDB; AAU11188.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need  
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.  
PT infections such as bacterial, fungal, protozoan and viral infections and  
PT cancers.

XX

PS Disclosure; Fig 5; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or  
CC its variant, encoded by the 8 exon sequences given in the specification.

CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the  
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is

CC administered by providing to the patient DNA encoding HFGAN72 and  
 CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly  
 CC useful for applications in the detection and treatment of disease, e.g.  
 CC infections such as bacterial, fungal, protozoan and viral infections,  
 CC particularly infections caused by human immunodeficiency virus (HIV)-1 or  
 CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial  
 CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,  
 CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,  
 CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),  
 CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,  
 CC Huntington's disease and many other diseases and disorders given in the  
 CC specification. The present sequence is the coding sequence of an  
 CC alternative allele of the human HFGAN72 receptor

XX

SQ Sequence 1564 BP; 267 A; 514 C; 437 G; 346 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 4; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-288;  
 Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600

Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCGCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTCCGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC	1233
Qy	1081	CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1234	CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1293
Qy	1141	GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1294	GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1353
Qy	1201	TCCTTGCAAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1260
Db	1354	TCCTTGCAAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1413
Qy	1261	ACCACAGTGCTGCCCTGA	1278
Db	1414	ACCACAGTGCTGCCCTGA	1431

RESULT 5

AAF32103

ID AAF32103 standard; cDNA; 1564 BP.

XX

AC AAF32103;

XX  
 DT 10-APR-2001 (first entry)  
 XX  
 DE Human HFGAN72 receptor coding sequence SEQ ID NO: 12.  
 XX  
 KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;  
 KW truncation mutant; ligand; neurodegenerative disorder; pain;  
 KW eating disorder; behaviour disorder; mood disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200100787-A2.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 22-JUN-2000; 2000WO-US017251.  
 XX  
 PR 25-JUN-1999; 99US-0141156P.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;  
 XX  
 DR WPI; 2001-071483/08.  
 XX  
 PT Polynucleotides encoding Lig 72A polypeptides or their variants, which  
 PT are useful in the treatment of a disease or disorder associated with  
 PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,  
 PT neuropathic pain and back pain.  
 XX  
 PS Disclosure; Fig 6; 101pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences for the  
 CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides  
 CC truncated mutant versions. These, and their agonists and antagonists, are  
 CC all useful in the treatment of eating, neurodegenerative, behaviour,  
 CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy  
 CC and acute inflammatory conditions  
 XX  
 SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 4; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-288;  
 Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213  
 Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273  
 Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333



Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCTGCTTC	1020
Db	1114	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCTGCTTC	1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 Qy 1081 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1234 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353  
 Qy 1201 TCCTTGCAAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||  
 Db 1354 TCCTTGCAAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413  
 Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431

# RESULT 6

ABA96021

ID ABA96021 standard; cDNA; 1564 BP.

XX

AC ABA96021;

XX

DT 12-MAR-2002 (first entry)

XX

DE HGS EST 554692.

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;  
 KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;  
 KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;  
 KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;  
 KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;  
 KW schizophrenia; manic depression; dementia; mental retardation; EST;  
 KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;  
 KW HGS EST 554692; expressed sequence tag; probe; ss.

XX

OS Homo sapiens.

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203010.

XX

PR 30-APR-1997; 97US-00846705.

PR 27-OCT-1997; 97EP-00308554.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-084320/12.

XX

PT New polynucleotide encoding a G-protein coupled receptor designated  
PT HFGAN72Y is useful to diagnose and treat associated diseases including  
PT cancer, infection, cardiac disease and psychotic and neurological  
PT disorders.

XX

PS Example 1; Page 19-20; 22pp; English.

XX

CC The sequence represents HGS EST 554692. The sequence was used in the  
CC invention as a probe to screen a human genomic placenta phage library.  
CC The invention relates to a novel isolated polynucleotide encoding  
CC HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic,  
CC cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti  
CC -asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y  
CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a  
CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y  
CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y  
CC expression is used to treat a subject in need of decreased HFGAN72Y  
CC activity or expression. HFGAN72Y-associated diseases include infections,  
CC particularly by HIV-1 or HIV-2, pain, anorexia, bulimia, Parkinson's  
CC disease, cardiac diseases, cancers, ulcers, urinary retention, asthma,  
CC allergies, benign prostatic hypertrophy, and psychotic and neurological  
CC disorders including anxiety, schizophrenia, manic depression, delirium,  
CC dementia, severe mental retardation and dyskinesias such as Huntington's  
CC disease and Tourette's syndrome

XX

SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;  
Best Local Similarity 99.8%; Pred. No. 1.9e-288;  
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60  
|  
Db 154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213  
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
|  
Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273  
Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180  
|  
Db 274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333  
Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
|  
Db 334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393  
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
|  
Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453  
Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
|  
Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513  
Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
|

Db 514 GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573  
 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633  
 Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813  
 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1233  
 Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353  
 Qy 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1354 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413



XX  
PS Example 3; Page 9; 24pp; English.

XX  
CC The present sequence is that of a known partial nucleotide sequence  
CC encoding a HFGAN72X polypeptide (AAG78346) used as a probe to identify  
CC the HFGAN72X gene (AAI64173). The specification describes a newly  
CC isolated polynucleotide encoding a human HFGAN72X G coupled receptor  
CC polypeptide. The protein of the invention has antibacterial, fungicide,  
CC virucide, protozoacide, anti-HIV, cardiant, analgesic, cytostatic,  
CC nootropic, antiparkinsonian, antiulcer, antiasthmatic, tranquiliser,  
CC neuroleptic, antidepressant, anticonvulsant and osteopathic activities.  
CC HFGAN72X polynucleotides (PNs) are used to express HFGAN72X in vivo, to  
CC treat diseases requiring increased activity or expression of HFGAN72X;  
CC for recombinant production of HFGAN72X; diagnose diseases by detecting  
CC mutations in genomic sequences and in chromosome identification and  
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as  
CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to  
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X  
CC PNs are used to identify (ant)agonists of HFGAN72X, useful  
CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and  
CC polypeptides that compete with ligands for binding to HFGAN72X proteins  
CC are also useful therapeutically and diagnostically. HFGAN72X-related  
CC diseases include infections (bacterial, viral, fungal or protozoal,  
CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's  
CC disease; acute heart failure; hypotension; hypertension; urinary  
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;  
CC manic depression; delirium; dementia; severe mental retardation and  
CC dyskinesias

Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;  
Best Local Similarity 99.8%; Pred. No. 1.9e-288;  
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360

Db	454		CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661		ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCG	720
Db	814		ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCG	873
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874		AAGCTCTGGGGCCGCCAGATCCCCGGCACCCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	993
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1080
Db	1174		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1233
Qy	1081		CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1234		CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1293
Qy	1141		GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200

Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 ||||| |||||||||||||||||||||||||||||||||||||||||

Db 1354 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||||||||||||||

Db 1414 ACCACAGTGCTGCCCTGA 1431

RESULT 8

AAI64172

ID AAI64172 standard; cDNA; 1564 BP.

XX

AC AAI64172;

XX

DT 22-JAN-2002 (first entry)

XX

DE Human HFGAN72X G coupled receptor polypeptide cDNA.

XX

KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;  
 KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;  
 KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;  
 KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;  
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;  
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;  
 KW ulcers; asthma; allergy; delirium; dementia;  
 KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;  
 KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 154..1431

FT /\*tag= a

FT /product= "HFGAN72X protein"

FT /note= "G coupled receptor polypeptide"

XX

PN EP1154019-A2.

XX

PD 14-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203008.

XX

PR 30-APR-1997; 97US-00846704.

PR 27-OCT-1997; 97EP-00308563.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-012659/02.

DR P-PSDB; AAG78345.

XX

PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and  
 PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's



PT disease, and acute heart failure.

XX

PS Claim 3; Page 7; 24pp; English.

XX

CC The present sequence is that of a cDNA encoding a HFGAN72X polypeptide  
CC (AAG78345). The specification describes a newly isolated polynucleotide  
CC encoding a HFGAN72X G coupled receptor polypeptide. The protein of the  
CC invention has antibacterial, fungicide, virucide, protozoacide, anti-HIV,  
CC cardiant, analgesic, cytostatic, nootropic, antiparkinsonian, antiulcer,  
CC antiasthmatic, tranquiliser, neuroleptic, antidepressant, anticonvulsant  
CC and osteopathic activities. HFGAN72X polynucleotides (PNs) are used to  
CC express HFGAN72X in vivo, to treat diseases requiring increased activity  
CC or expression of HFGAN72X; for recombinant production of HFGAN72X;  
CC diagnose diseases (or susceptibility to them) by detecting mutations in  
CC genomic sequences and in chromosome identification and mapping. HFGAN72X  
CC polypeptides are used to raise specific antibodies; as therapeutic agents  
CC ; to identify HFGAN72X protein-expressing clones; to purify HFGAN72X  
CC proteins; in vaccines. Cells transformed with HFGAN72X PNs are used to  
CC identify (ant)agonists of HFGAN72X, useful therapeutically. Nucleic acids  
CC that inhibit expression of HFGAN72X and polypeptides that compete with  
CC ligands for binding to HFGAN72X proteins are also useful therapeutically  
CC and diagnostically. HFGAN72X-related diseases include infections  
CC (bacterial, viral, fungal or protozoal, particularly HIV-1 or -2); pain;  
CC cancer; anorexia; bulimia; Parkinson's disease; acute heart failure;  
CC hypotension; hypertension; urinary retention; osteoporosis; angina  
CC pectoris; myocardial infarction; ulcers; asthma; allergy; benign  
CC prostatic hypertrophy; anxiety; schizophrenia; manic depression; delirium  
CC ; dementia; severe mental retardation and dyskinesias

XX

SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;  
Best Local Similarity 99.8%; Pred. No. 1.9e-288;  
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60  
|  
Db 154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213  
  
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
|  
Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273  
  
Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180  
|  
Db 274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333  
  
Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
|  
Db 334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393  
  
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
|  
Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453  
  
Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360  
|

Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513  
 Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573  
 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633  
 Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813  
 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 814 ATTGTACCTACCTGGCCCCACTGGGCCATGGCCATGGCCTATTTCCAGATATTCCGC 873  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1233  
 Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy 1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||  
 Db 1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413  
 Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431

RESULT 9

ABZ42789

ID ABZ42789 standard; DNA; 1564 BP.

XX

AC ABZ42789;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human orexin receptor 1 nucleotide SEQ ID NO:367.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR

P-PSDB; ABP81941.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising: (a)

any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

XX

SQ Sequence 1564 BP; 268 A; 513 C; 436 G; 347 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 7; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-288;  
 Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
      |||
Db      154 ATGGAGCCCTCAGCCACCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      |||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGGCC 180
      |||
Db      274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
      |||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
      |||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
      |||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATC 420
      |||

```

Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTACCTACCTGGCCCCACTGGGCCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1233
Qy	1081	CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1234	CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1293
Qy	1141	GGTCCCTGCGGCTCTCTGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1294	GGTCCCTGCGGCTCTCTGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1353
Qy	1201	TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1260
Db	1354	TCCTTGAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1413

RESULT 10

ABI98014

ID ABI98014 standard; cDNA; 1278 BP.

XX

AC ABI98014;

XX

DT 18-FEB-2002 (first entry)

XX

DE Non-endogenous human GPCR cDNA, SEQ ID NO: 548.

XX

KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;  
KW constitutively activated GPCR; agonist; disease; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200177172-A2.

XX

PD 18-OCT-2001.

XX

PF 05-APR-2001; 2001WO-US011098.

XX

PR 07-APR-2000; 2000US-0195747P.

XX

PA (AREN-) ARENA PHARM INC.

XX

PI    Lehmann-B Bruinsma K,    Liaw CW,    Lin I;

XX

DR WPI; 2001-648759/74.

DR P-PSDB; ABB56378.

XX

PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in  
PT disease treatment, comprises contacting candidate compounds with versions  
PT of GPCRs.

XX

PS Example 2; Page 349-350; 394pp; English.

XX

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous constitutively  
CC activated versions of known GPCRs are used in the invention for the  
CC direct identification of candidate compounds as receptor agonists,  
CC inverse agonists or partial agonists. Such agonists are useful as  
CC therapeutic agents for diseases or disorders associated with GPCRs. The  
CC present sequence encodes a non-endogenous version of a known human GPCR

XX

SQ Sequence 1278 BP; 224 A; 423 C; 346 G; 285 T; 0 U; 0 Other;

Query Match 99.4%; Score 1270; DB 5; Length 1278;

Best Local Similarity 99.6%; Pred. No. 2.3e-287;

Matches 1273; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60  
 |||  
 Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
 |||  
 Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180  
 |||  
 Db 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180

Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 |||  
 Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 |||  
 Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 |||  
 Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||  
 Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||  
 Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540  
 |||  
 Db 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||  
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 |||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Db	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAGATGCTG	900
Qy	901		ATGGTGGTGTCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901		ATGGTGGTGTCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1080
Db	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1080
Qy	1081		CTCAGTGGCAAATTCCGGGAGCAGTTTAAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1081		CTCAGTGGCAAATTCCGGGAGCAGTTTAAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Qy	1141		GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1141		GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Qy	1201		TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1260
Db	1201		TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1260
Qy	1261		ACCACAGTGCTGCCCTGA	1278
Db	1261		ACCACAGTGCTGCCCTGA	1278

RESULT 11

AAD09335

ID AAD09335 standard; cDNA; 1278 BP.

XX

AC AAD09335;

XX

DT 10-SEP-2001 (first entry)

XX

DE Cynomolgous Monkey Orexin 1 Receptor cDNA.

XX

KW Cynomolgous monkey; Orexin 1 Receptor; 7 Transmembrane Receptor family;

KW 7TM; gene therapy; vaccine; microbial infection; HIV-1; HIV-2; pain;

KW cancer; diabetes; obesity; anorexia; bulimia; urinary retention;

KW Parkinson's disease; acute heart failure; hypotension; hypertension;

KW osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer;

KW asthma; allergy; benign prostatic hypertrophy; migraine; vomiting;

KW psychotic disorder; neurological disorder; anxiety; schizophrenia;

KW manic depression; depression; delirium; dementia; mental retardation;

KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; ss.

XX

OS Macaca fascicularis.

XX

FH Key Location/Qualifiers

FT CDS 1. .1278

FT /\*tag= a



FT /product= "Orexin 1 Receptor"

XX

PN WO200140259-A2.

XX

PD 07-JUN-2001.

XX

PF 04-DEC-2000; 2000WO-US032849.

XX

PR 02-DEC-1999; 99US-0168553P.

PR 28-NOV-2000; 2000US-00723781.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Ellis CE;

XX

DR WPI; 2001-408276/43.

DR P-PSDB; AAE04740.

XX

PT Novel Cynomolgous Monkey Orexin 1 Receptor polypeptides, for treating

PT infections, pain, cancer, diabetes, obesity, asthma, schizophrenia,

PT hypertension, urinary retention, Parkinson's disease and stroke.

XX

PS Claim 1; Page 28; 33pp; English.

XX

CC The present sequence is a cDNA encoding Cynomolgous Monkey Orexin 1  
CC Receptor which is structurally related to members of 7 Transmembrane  
CC Receptor (7TM) family. The Orexin 1 Receptor polypeptide and  
CC polynucleotide are useful for treating bacterial, fungal, protozoan and  
CC viral infections, particularly infections caused by HIV-1 or HIV-2, pain,  
CC cancer, diabetes, obesity, anorexia, bulimia, Parkinson's disease, acute  
CC heart failure, hypotension, hypertension, urinary retention,  
CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers,  
CC asthma, allergies, benign prostatic hypertrophy, migraine, vomiting,  
CC psychotic and neurological disorders including anxiety, schizophrenia,  
CC manic depression, depression, delirium, dementia and severe mental  
CC retardation, and dyskinesias, such as Huntington's disease or Gilles de  
CC la Tourette's syndrome. The polypeptide is also useful for structure-  
CC based design of its agonist, antagonist or inhibitor. The polynucleotide  
CC is useful for chromosome localisation studies and in gene therapy. The  
CC Orexin 1 Receptor polypeptide and polynucleotide are also useful as  
CC vaccines

XX

SQ Sequence 1278 BP; 219 A; 433 C; 346 G; 280 T; 0 U; 0 Other;

Query Match 95.9%; Score 1225.2; DB 4; Length 1278;

Best Local Similarity 97.4%; Pred. No. 7.1e-277;

Matches 1245; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

|||||

Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGCGGGTCCCCACTGGCAGCAGGGAGCCA 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

|||||

Db 61 TCCCCTGTGCCTCCAGACTATGAAGACGAGTTTCTCCGCTACCTGTGGCGCGATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
 |||  
 Db 121 TACCCAAAACAGTACGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCCTCGTGGCC 180

Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 |||  
 Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGA CTGCTATCTGCCTG 300  
 |||  
 Db 241 ACCAACTACTTCATCGTCAACCTGTCCCTGGCTGACGTTCTGGTAACTGCCATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 |||  
 Db 301 CCGGTACGCTGCTGGTGGACATCACTGAGTCTGGCTGTTTCGGCCATGCTCTCTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||  
 Db 361 GTCATCCCCTATCTACAGGCCGTGTCCGTGTGAGTGGCAGTGCTGACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||  
 Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 |||  
 Db 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCTGTATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||  
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCGCGAGCTAGCCAACCGCACACGGCTCTTCTCG 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTATATCCCAAGATCTACCACAGTTGCTTCTTC 660

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 |||  
 Db 721 AAGCTCTGGGGCCGCCAGATTCCCGGCACCACTCAGCACTGGTGCGAAAGTGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGACAGCCCCAGCCCCGGGCC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGTGTCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

```

          |||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
          |||
QY      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
          |||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGTGCTGCCAACCCCATCATCTACAACCTTC 1080
          |||
QY      1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
          |||
Db      1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCCG 1140
          |||
QY      1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
          |||
Db      1141 GGCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
          |||
QY      1201 TCCTTGCCAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
          |||
Db      1201 TCCTTGCCAGAGCCGATGCTCCGTCTCCAACTCTCTGAGCACGTGGTGCTCACCAGCGTC 1260
          |||
QY      1261 ACCACAGTGCTGCCCTGA 1278
          |||
Db      1261 ACCACAGTGCTGCCCTGA 1278

```

# RESULT 12

AAT42826

ID AAT42826 standard; cDNA; 1209 BP.

XX

AC AAT42826;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor gene.

XX

KW Human; neuropeptide receptor; drug screening; receptor-agonist;

KW receptor-antagonist; anorectic; antitumour; anticholesterolemic;

KW neuroprotective; anticonvulsant; hypotensive; sedative; diagnostic;

KW gene therapy; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT primer\_bind complement(1..18)

FT /\*tag= a

FT /note= "Binds primer AAT42829"

FT misc\_difference 151..153

FT /\*tag= b

FT /codon= seq:CCA, aa:Ala

FT primer\_bind complement(1190..1192)

FT /\*tag= c

FT /note= "Binds primers AAT42830 and AAT42832"

XX

PN WO9634877-A1.

XX

PD 07-NOV-1996.

XX

PF 05-MAY-1995; 95WO-US005616.

XX 05-MAY-1995; 95WO-US005616.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Soppet DR, Li Y, Rosen CA;  
XX  
DR WPI; 1996-506094/50.  
DR P-PSDB; AAW06124.  
XX  
PT Human neuro-peptide receptor polypeptide(s) - used to identify  
PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of  
PT obesity, Alzheimer's disease, epilepsy, etc.  
XX  
PS Claim 6; Page 48-49; 77pp; English.  
XX  
CC The sequence encodes a human neuropeptide receptor, and has been mapped  
CC to human chromosome 1q31-34. The sequence has been isolated from a human  
CC adult hypothalamus cDNA library, and is structurally related to the G-  
CC protein-coupled receptor family. Splice variants are given in AAT42827-  
CC 28. The sequence may be amplified by PCR with e.g. primers AAT42829-34  
CC for expression in a host cell. The recombinant receptor may be used in a  
CC drug screening assay for isolation of receptor-agonists and -antagonists,  
CC which may be used as anorectic, antitumour, anticholesterolemic,  
CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The  
CC DNA may also be used in genetic disease diagnosis or gene therapy. The  
CC receptor and its corresponding antibody may also be used in therapy and  
CC diagnosis  
XX  
SQ Sequence 1209 BP; 206 A; 402 C; 330 G; 271 T; 0 U; 0 Other;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360

Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361		420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421		480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481		540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541		600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601		660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661		720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721		780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781		840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841		900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901		960
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961		1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1080
Db	1021		1080
Qy	1081	CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1081		1140
Qy	1141	GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1141		1200

Qy 1201 TCCTTGCAg 1209  
      ||||| II  
Db 1201 TCCTTGTAG 1209

RESULT 13

AAV68512

ID AAV68512 standard; cDNA; 1133 BP.

XX

AC AAV68512;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of HGS EST 557082.

XX

KW HGS EST 557082; G-protein coupled receptor family; HFGAN72Y; mutation;  
KW probe; agonist; antagonist; activation; inhibition; gene therapy;  
KW antibody; immune response; vaccine; HIV-1; HIV-2; cancer; anorexia;  
KW bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;  
KW hypertension; urinary retention; osteoporosis; angina pectoris;  
KW myocardial infarction; ulcer; allergies; psychotic disorder;  
KW neurological disorder; gene mapping; ss.

XX

OS Homo sapiens.

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX

PR 30-APR-1997; 97US-00846705.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis C;

XX

DR WPI; 1998-570286/49.

XX

PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -  
PT useful as diagnostic reagents and for prevention and treatment of HIV  
PT infections, cancer, osteoporosis and Parkinson's disease.

XX

PS Example 1; Page 18-19; 22pp; English.

XX

CC This is the nucleotide sequence of the HGS EST 557082 used in the method  
CC of the invention involving the G-protein coupled receptor, HFGAN72Y. Its  
CC polypeptides and polynucleotides are useful for diagnosing susceptibility  
CC to diseases by detecting mutations in the HFGAN72Y gene using probes  
CC containing the HFGAN72Y nucleotide sequence, and can diagnose diseases  
CC associated with HFGAN72Y imbalance by determining HFGAN72Y polypeptide or  
CC mRNA expression levels. Agonists/antagonists can be used in treatment to  
CC activate/inhibit HFGAN72Y activity, in addition to direct administration  
CC of antisense sequences to prevent expression, or HFGAN72Y polypeptides to  
CC treat conditions associated with a lack HFGAN72Y protein. Gene therapy  
CC may also be used to affect endogenous HFGAN72Y polypeptide production.

CC HFGAN72Y antibodies are useful for inducing an immune response to  
 CC immunise and prevent diseases, and for isolating HFGAN72Y clones or  
 CC purifying the polypeptides by affinity chromatography. HFGAN72Y  
 CC polypeptides can be administered directly or as a vaccine to inoculate  
 CC against diseases. Diseases diagnosed, prevented or treated include HIV-1  
 CC or HIV-2 infections, pain, cancers, anorexia, bulimia, asthma,  
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,  
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,  
 CC ulcers; allergies, benign prostatic hypertrophy, and psychotic and  
 CC neurological disorders. The HFGAN72Y polypeptide is also useful for  
 CC mapping the gene to a chromosome, allowing gene inheritance to be studied  
 CC through linkage analysis

XX

SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 85.0%; Score 1086.4; DB 2; Length 1133;  
 Best Local Similarity 99.9%; Pred. No. 2.1e-244;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600

Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGG 1088  
 ||||||||  
 Db 1081 CTCAGTGG 1088

RESULT 14

ABA96020

ID ABA96020 standard; cDNA; 1133 BP.

XX

AC ABA96020;

XX

DT 12-MAR-2002 (first entry)

XX

DE HGS EST 557082.

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;  
 KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;  
 KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;  
 KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;  
 KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;  
 KW schizophrenia; manic depression; dementia; mental retardation; EST;  
 KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;  
 KW HGS EST 557082; expressed sequence tag; ss.



XX  
 OS Homo sapiens.  
 XX  
 PN EP1156110-A2.  
 XX  
 PD 21-NOV-2001.  
 XX  
 PF 27-OCT-1997; 2001EP-00203010.  
 XX  
 PR 30-APR-1997; 97US-00846705.  
 PR 27-OCT-1997; 97EP-00308554.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Bergsma DJ, Ellis CE;  
 XX  
 DR WPI; 2002-084320/12.  
 XX  
 PT New polynucleotide encoding a G-protein coupled receptor designated  
 PT HFGAN72Y is useful to diagnose and treat associated diseases including  
 PT cancer, infection, cardiac disease and psychotic and neurological  
 PT disorders.  
 XX  
 PS Example 1; Page 18-19; 22pp; English.  
 XX  
 CC The sequence represents HGS EST 557082. The invention relates to a novel  
 CC isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of  
 CC the invention has cytostatic, cardiant, analgesic, tranquillising,  
 CC nootropic, neuroprotective, and anti-asthmatic activity. The HFGAN72Y has  
 CC a use in gene therapy. The HFGAN72Y polynucleotide or an HFGAN72Y  
 CC polypeptide agonist are used to treat a subject in need of enhanced  
 CC HFGAN72Y activity or expression. An HFGAN72Y antagonist or competitor, or  
 CC nucleic acid which inhibits HFGAN72Y expression is used to treat a  
 CC subject in need of decreased HFGAN72Y activity or expression. HFGAN72Y-  
 CC associated diseases include infections, particularly by HIV-1 or HIV-2,  
 CC pain, anorexia, bulimia, Parkinson's disease, cardiac diseases, cancers,  
 CC ulcers, urinary retention, asthma, allergies, benign prostatic  
 CC hypertrophy, and psychotic and neurological disorders including anxiety,  
 CC schizophrenia, manic depression, delirium, dementia, severe mental  
 CC retardation and dyskinesias such as Huntington's disease and Tourette's  
 CC syndrome  
 XX  
 SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 85.0%; Score 1086.4; DB 6; Length 1133;  
 Best Local Similarity 99.9%; E-Value No. 2.1e-244;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180

Db	121		TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGGCC	180
Qy	181		CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181		CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241		ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241		ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301		CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301		CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACTGGAAGCGC	780
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961		AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020

Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||

Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080

Qy 1081 CTCAGTGG 1088  
 |||

Db 1081 CTCAGTGG 1088

RESULT 15

AAV68511

ID AAV68511 standard; cDNA; 1170 BP.

XX

AC AAV68511;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of HFGAN72Y a G-protein coupled receptor.

XX

KW G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;  
 KW antagonist; activation; inhibition; gene therapy; antibody;  
 KW immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;  
 KW asthma; Parkinson's disease; acute heart failure; hypotension;  
 KW hypertension; urinary retention; osteoporosis; angina pectoris;  
 KW myocardial infarction; ulcer; allergies; psychotic disorder;  
 KW neurological disorder; gene mapping; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .1170

FT /\*tag= a

FT /product= "HFGAN72Y protein"

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX

PR 30-APR-1997; 97US-00846705.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis C;

XX

DR WPI; 1998-570286/49.

DR P-PSDB; AAW80805.

XX

PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -  
 PT useful as diagnostic reagents and for prevention and treatment of HIV  
 PT infections, cancer, osteoporosis and Parkinson's disease.

XX

PS Claim 3; Page 7; 22pp; English.

XX

CC This is the nucleotide sequence of the G-protein coupled receptor,  
CC HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and  
CC polynucleotides are useful for diagnosing susceptibility to diseases by  
CC detecting mutations in the HFGAN72Y gene using probes containing the  
CC HFGAN72Y nucleotide sequence, and can diagnose diseases associated with  
CC HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression  
CC levels. Agonists/antagonists can be used in treatment to activate/inhibit  
CC HFGAN72Y activity, in addition to direct administration of antisense  
CC sequences to prevent expression, or HFGAN72Y polypeptides to treat  
CC conditions associated with a lack HFGAN72Y protein. Gene therapy may also  
CC be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y  
CC antibodies are useful for inducing an immune response to immunise and  
CC prevent diseases, and for isolating HFGAN72Y clones or purifying the  
CC polypeptides by affinity chromatography. HFGAN72Y polypeptides can be  
CC administered directly or as a vaccine to inoculate against diseases.  
CC Diseases diagnosed, prevented or treated include HIV-1 or HIV-2  
CC infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's  
CC disease, acute heart failure, hypotension, hypertension, urinary  
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;  
CC allergies, benign prostatic hypertrophy, and psychotic and neurological  
CC disorders. The HFGAN72Y polypeptide is also useful for mapping the gene  
CC to a chromosome, allowing gene inheritance to be studied through linkage  
CC analysis

XX

SQ Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

Query Match 85.0%; Score 1086.4; DB 2; Length 1170;  
Best Local Similarity 99.9%; Pred. No. 2.1e-244;  
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60  
|  
Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60  
  
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
|  
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
  
Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
|  
Db 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
  
Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
|  
Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
  
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
|  
Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
  
Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
|  
Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
  
Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
|  
Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||  
 Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCT 540  
 |||  
 Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||  
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 |||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy 1081 CTCAGTGG 1088  
 |||  
 Db 1081 CTCAGTGG 1088

Search completed: October 15, 2004, 16:01:42  
 Job time : 550.899 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:25:17 ; Search time 100.178 Seconds  
(without alignments)  
7079.645 Million cell updates/sec

Title: US-10-070-532-1  
Perfect score: 1278  
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgcctgcctga 1278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query			Description
	Score	Match	Length	DB	ID	
1	1274.8	99.7	1564	2	US-08-846-705-4	Sequence 4, Appli
2	1274.8	99.7	1564	3	US-08-846-704-1	Sequence 1, Appli
3	1274.8	99.7	1564	3	US-08-846-704-3	Sequence 3, Appli
4	1205.8	94.4	1209	4	US-08-462-509B-1	Sequence 1, Appli
5	1201	94.0	1209	5	PCT-US95-05616-1	Sequence 1, Appli
6	1086.4	85.0	1133	2	US-08-846-705-3	Sequence 3, Appli
7	1086.4	85.0	1170	2	US-08-846-705-1	Sequence 1, Appli
8	1085.8	85.0	1110	4	US-08-462-509B-3	Sequence 3, Appli
9	1083.2	84.8	1116	4	US-08-462-509B-5	Sequence 5, Appli
10	1083.2	84.8	1133	5	PCT-US95-05616-5	Sequence 5, Appli
11	1077.8	84.3	1110	5	PCT-US95-05616-3	Sequence 3, Appli

12	699.2	54.7	843	3	US-08-513-974B-375	Sequence 375, App
13	672.2	52.6	789	3	US-08-513-974B-55	Sequence 55, Appl
14	672.2	52.6	789	4	US-09-461-436B-55	Sequence 55, Appl
15	554.4	43.4	1633	3	US-09-119-788-1	Sequence 1, Appli
16	249.2	19.5	9785	4	US-09-479-128-1	Sequence 1, Appli
17	188.8	14.8	1287	2	US-08-846-705-5	Sequence 5, Appli
18	163.2	12.8	1293	3	US-09-255-368-7	Sequence 7, Appli
19	156.2	12.2	1410	3	US-09-255-368-1	Sequence 1, Appli
20	128.4	10.0	168575	4	US-09-426-290-1	Sequence 1, Appli
21	119	9.3	1110	3	US-08-513-974B-31	Sequence 31, Appl
22	119	9.3	1110	3	US-08-776-971-26	Sequence 26, Appl
23	119	9.3	1110	4	US-09-461-436B-31	Sequence 31, Appl
24	119	9.3	1331	3	US-08-513-974B-322	Sequence 322, App
25	119	9.3	1331	3	US-08-776-971-103	Sequence 103, App
26	108.8	8.5	669	3	US-08-513-974B-314	Sequence 314, App
27	108.8	8.5	669	3	US-08-776-971-99	Sequence 99, Appl
28	108.8	8.5	1113	3	US-09-172-353-1	Sequence 1, Appli
29	108.8	8.5	1113	4	US-09-799-955-1	Sequence 1, Appli
30	103.2	8.1	1110	4	US-09-170-496D-25	Sequence 25, Appl
31	103.2	8.1	1110	4	US-09-170-496D-177	Sequence 177, App
32	103.2	8.1	1344	4	US-09-016-434-1295	Sequence 1295, Ap
33	103.2	8.1	1356	1	US-07-978-892A-4	Sequence 4, Appli
34	103.2	8.1	1535	4	US-09-016-434-1051	Sequence 1051, Ap
35	103.2	8.1	1969	1	US-07-937-609-28	Sequence 28, Appl
36	103.2	8.1	1969	3	US-08-029-170-28	Sequence 28, Appl
37	100	7.8	2243	1	US-07-937-609-15	Sequence 15, Appl
38	100	7.8	2243	3	US-08-029-170-15	Sequence 15, Appl
39	98.4	7.7	1621	1	US-08-722-001-13	Sequence 13, Appl
40	98.4	7.7	1776	1	US-08-722-001-29	Sequence 29, Appl
41	98.4	7.7	2002	4	US-09-016-434-1172	Sequence 1172, Ap
42	98.4	7.7	2140	1	US-08-334-698-1	Sequence 1, Appli
43	98.4	7.7	2140	1	US-08-228-932-1	Sequence 1, Appli
44	98.4	7.7	2140	1	US-08-468-939-1	Sequence 1, Appli
45	98.4	7.7	2140	2	US-08-406-855A-1	Sequence 1, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-846-705-4

; Sequence 4, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette





Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573  
 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633  
 Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813  
 Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1233  
 Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353  
 Qy 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1354 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

| | | | |

US-08-846-704-1

GENERAL INFORMATION:

APPLICANT: BERGSMA, DERK J.

APPLICANT: ELLIS, CATHERINE E.

TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RATNER & PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/846,704

FILING DATE: 30-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-70002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1564 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US--08-846-704-1

Query Match 99.7%; Score 1274.8; DB 3; Length 1564;  
Best Local Similarity 99.8%; Pred. No. 3.2e-287;  
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

\_\_\_\_\_

Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213  
 Qy 61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 214 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273  
 Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 333  
 Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393  
 Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453  
 Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513  
 Qy 361 GTCATCCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 514 GTCATCCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573  
 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633  
 Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813  
 Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080  
 |||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233  
 Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353  
 Qy 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||  
 Db 1354 TCCTTGAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413  
 Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431

RESULT 3

US-08-846-704-3

; Sequence 3, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,704

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-704-3

```

```

Query Match          99.7%; Score 1274.8; DB 3; Length 1564;
Best Local Similarity 99.8%; Pred. No. 3.2e-287;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1 ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTGCCCCAGGCT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTGCCCCAGGCT 693

```

Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGTGCCAACCCCATCATCTACAACCTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGTGCCAACCCCATCATCTACAACCTC	1233
Qy	1081	CTCAGTGGCAAATTCGGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1234	CTCAGTGGCAAATTCGGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1293
Qy	1141	GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1294	GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1353
Qy	1201	TCCTTGCGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1260
Db	1354	TCCTTGCGAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1413
Qy	1261	ACCACAGTGCTGCCCTGA	1278
Db	1414	ACCACAGTGCTGCCCTGA	1431

RESULT 4

US-08-462-509B-1

; Sequence 1, Application US/08462509B



Db 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
 Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC 420  
 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 Qy 481 GCCCCTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 481 GCCCCTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020



Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 Qy 1201 TCCTTGAG 1209  
 |||  
 Db 1201 TCCTTGAG 1209

RESULT 5

PCT-US95-05616-1

; Sequence 1, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05616

; FILING DATE: concurrently

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-268

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1209 BASE PAIRS

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: cDNA

PCT-US95-05616-1

Query Match 94.0%; Score 1201; DB 5; Length 1209;  
 Best Local Similarity 99.6%; Pred. No. 4.2e-270;  
 Matches 1204; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721	AACCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACTGGAAGCGC	780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 Qy 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1141 GGTCCCTGCGGCTCTCTGAAGGCCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 Qy 1201 TCCTTGCA 1209  
 |||  
 Db 1201 TCCTTGTA 1209

RESULT 6

US-08-846-705-3

; Sequence 3, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,705

; FILING DATE: 30-APR-1997

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-705-3

```

```

Query Match          85.0%; Score 1086.4; DB 2; Length 1133;
Best Local Similarity 99.9%; Pred. No. 1.8e-243;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGA CTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGA CTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

```

Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT	1080
Qy	1081	CTCAGTGG	1088
Db	1081	CTCAGTGG	1088

# RESULT 7

US-08-846-705-1

; Sequence 1, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

```

; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-705-1

```

```

Query Match      85.0%; Score 1086.4; DB 2; Length 1170;
Best Local Similarity 99.9%; Pred. No. 1.8e-243;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

```

Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTACCTACCTGGCCCCACTGGGCCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Qy	1081	CTCAGTGG	1088
Db	1081	CTCAGTGG	1088

RESULT 8

US-08-462-509B-3

; Sequence 3, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1110 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1110

US-08-462-509B-3

Query Match 85.0%; Score 1085.8; DB 4; Length 1110;

Best Local Similarity 99.8%; Pred. No. 2.4e-243;

Matches 1087; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

|||||

Db 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

|||||

Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120



Qy	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Qy 1081 CTCAGTGGC 1089  
 |||  
 Db 1081 CTCAGTGGC 1089

RESULT 9

US-08-462-509B-5

; Sequence 5, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1116 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1116

Query Match 84.8%; Score 1083.2; DB 4; Length 1116;  
Best Local Similarity 99.7%; Pred. No. 9.7e-243;  
Matches 1085; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCC	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC	780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGG 1088  
 ||||||||  
 Db 1081 CTCAGTGG 1088

RESULT 10

PCT-US95-05616-5

; Sequence 5, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05616

; FILING DATE: concurrently

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-268

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

```
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1133 BASE PAIRS
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: SINGLE
;   TOPOLOGY: LINEAR
;   MOLECULE TYPE: cDNA
PCT-US95-05616-5
```

```
Query Match          84.8%; Score 1083.2; DB 5; Length 1133;
Best Local Similarity 99.7%; Pred. No. 9.8e-243;
Matches 1085; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
      ||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      ||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180
      ||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
      ||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
      ||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
      ||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
      ||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
      ||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCGCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGCGCTGGCCATCATGGTGCGCCAGGCT 540
      ||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGCGCTGGCCATCATGGTGCGCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
      ||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
      ||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
```

Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACCTGGAAGCGC 780  
 |||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACCTGGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080

Qy 1081 CTCAGTGG 1088  
 |||  
 Db 1081 CTCAGTGG 1088

RESULT 11

PCT-US95-05616-3

; Sequence 3, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05616

; FILING DATE: concurrently

; CLASSIFICATION:

```

;   ATTORNEY/AGENT INFORMATION:
;   NAME:  FERRARO, GREGORY D.
;   REGISTRATION NUMBER:  36,134
;   REFERENCE/DOCKET NUMBER:  325800-268
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  201-994-1700
;   TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1110 BASE PAIRS
;   TYPE:  NUCLEIC ACID
;   STRANDEDNESS:  SINGLE
;   TOPOLOGY:  LINEAR
;   MOLECULE TYPE:  cDNA
PCT-US95-05616-3

```

```

Query Match          84.3%;  Score 1077.8;  DB 5;  Length 1110;
Best Local Similarity 99.4%;  Pred. No. 1.7e-241;
Matches 1082;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

```

```

Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

```





; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,974B  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP95/01599  
; FILING DATE: 10-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-093989  
; FILING DATE: 19-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-057186  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-007177  
; FILING DATE: 20-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-326611  
; FILING DATE: 28-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-270017  
; FILING DATE: 02-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236357  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236356  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189274  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189273  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189272  
; FILING DATE: 11-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 45753  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 375:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 843 base pairs  
; TYPE: nucleic acid

```
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..816
US-08-513-974B-375
```

```
Query Match          54.7%; Score 699.2; DB 3; Length 843;
Best Local Similarity 90.0%; Pred. No. 1.6e-153;
Matches 749; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
```

```
Qy      252 CATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCT 311
      | | ||| ||||| ||||| || || ||||| || ||||| ||||| ||
Db      9   CGTGTTCATCCTGTCACTGGCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCT 68

Qy      312 GCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCTA 371
      ||||| ||||| || ||||| || ||||| ||||| ||||| ||||| ||
Db      69 GCTGGTAGACATCACGGAATCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTA 128

Qy      372 TCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCG 431
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      129 TCTACAGGCCGTGTCCGTGTCACTGGTCTGTGCTGACTCTCAGCTCCATCGCCCTGGACCG 188

Qy      432 CTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGGCGGGCCCGTGGCTC 491
      ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db      189 CTGGTACGCCATCTGCCACCCGCTGTTGTTCAAGAGCACTGCCCGGGCGGCGCCGCGGCTC 248

Qy      492 CATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGA 551
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      249 CATCCTCGGCATCTGGGCGGTGTGCTGGCTGTCATGGTGCCCTCAGGCTGCTGTCATGGA 308

Qy      552 ATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGA 611
      || ||||| ||||| ||||| ||||| ||||| || || || || ||||| ||
Db      309 GTGTAGCAGCGTGTGCTGCCCGAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGA 368

Qy      612 ACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTA 671
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      369 GCGCTGGGCAGACGACCTGTACCCCAAGATCTACCACAGCTGCTTCTTCATTGTACCTA 428

Qy      672 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGG 731
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      429 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGG 488

Qy      732 CCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACTGGAAGCGCCCTCAGACCA 791
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      489 CCGCCAGATCCCCGGCACCACTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCA 548

Qy      792 GCTGGGGGACCTGGAGCAGGGCCTGAGTGAGAGCCCCAGCCCCGGGCCCCGCGCCTTCCT 851
      ||||| |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      549 GCTGGACGACCAGGGCCAGGGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCCGCGCCTTCCT 608

Qy      852 GGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCT 911
      ||| || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||
Db      609 GGCCGAGGTGAAACAGATGCGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCT 668

Qy      912 GCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTT 971
```

```

          ||||||||||||||||||||||||||||||||||||||||
Db      669 GCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGTGTCTCAACGTCCTCAAGAGGGTCTT 728

QY      972 CGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCA 1031
          ||||||||||||||||||||||||||||||||||||||||
Db      729 CGGGATGTTCCGCCAAGCCAGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCA 788

QY      1032 CTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTC 1083
          ||||||||||||||||||||||||||||||||||||||||
Db      789 CTGGCTGGTGTACGCCAACAGCGCCGCCAATCCCCTCCTCTACTCCTTCCTC 840

```

RESULT 13

US-08-513-974B-55

; Sequence 55, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji

; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo

; APPLICANT: Ohtaki, Tetsuya

; APPLICANT: Fukusumi, Shoji

; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF

; NUMBER OF SEQUENCES: 380

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/513,974B

; FILING DATE: 14-SEP-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP95/01599

; FILING DATE: 10-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-093989

; FILING DATE: 19-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-057186

; FILING DATE: 16-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-007177

; FILING DATE: 20-JAN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 6-326611

; FILING DATE: 28-DEC-1994

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-513-974B-55

```

Query Match 52.6%; Score 672.2; DB 3; Length 789;  
Best Local Similarity 90.7%; Pred. No. 2.9e-147;  
Matches 716; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy	271	GCTGACGTTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGAACATACTGAG	330
Db	1	GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA	60
Qy	331	TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG	390
Db	61	TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG	120
Qy	391	TCA GTGGCAGT GCTA A CTCT CAGCT TCATCGCCCTGGACC GTGGTATGCCATCTGCCAC	450
Db	121	TCA GTGGT CGTGT GACTCTC AGCTCCATCGCCCTGGACC GTGGTACGCCATCTGCCAC	180
Qy	451	CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT	510
Db	181	CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCGCGGCTCCATCCTCGGCATCTGGGCG	240
Qy	511	GTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT	570
Db	241	GTGTGCTGGCTGTCATGGTGCTCAGGCTGCTGTGTCATGGAGTGTAGCAGCGTGTGCCC	300

Qy	571	GAGCTAGGCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTC	630
Db	301	GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG	360
Qy	631	TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTC	690
Db	361	TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTACCTACCTGGCCCCACTGGGCCTC	420
Qy	691	ATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC	750
Db	421	ATGGCCATGGCCTATTTCCAGATCTTCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC	480
Qy	751	ACCTCAGCACTGGTGCGGAAGTGAAGCGCCCTCAGACCAGCTGGGGGACCTGGAGCAG	810
Db	481	ACCTCGGCCCTGGTGCGCAAGTGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG	540
Qy	811	GGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG	870
Db	541	GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG	600
Qy	871	CGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGC	930
Db	601	CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGC	660
Qy	931	TACCTGCCCATCAGCGTCTCTCAATGTCCTTAAGAGGGTGTTCCGGATGTTCCGCCAAGCC	990
Db	661	TACCTGCCCATCAGTGTCTCTCAACGTCCTCAAGAGGGTGTTCCGGATGTTCCGCCAAGCC	720
Qy	991	AGTGACCGGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC	1050
Db	721	AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC	780
Qy	1051	AGCGCTGCC	1059
Db	781	AGCGCCGCC	789

US-09-461-436B-55

; Sequence 55, Application US/09461436B

; GENERAL INFORMATION:

APPLICANT: Shuji Hinuma

; Yasuaki Ito

Ryo Fujii

; TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
 ; Production, And Use Thereof

```
;      NUMBER OF SEQUENCES: 61
```

; ADDRESSEE: Edwards & Angell, LLP

CITY: BOSTON

; COUNTRY: USA

COMPUTER READABLE FORM:



Qy 331 TCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCCTATCTACAGGCTGTGTCCGTG 390  
 ||||| || |||||  
 Db 61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCCTATCTACAGGCCGTGTCCGTG 120

Qy 391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450  
 ||||| ||||| |||||  
 Db 121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy 451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510  
 || || ||||| ||||| ||||| |||||  
 Db 181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGGCTCCATCCTCGGCATCTGGGCG 240

Qy 511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570  
 ||||| ||||| ||||| |||||  
 Db 241 GTGTCGCTGGCTGTCATGGTGCCCTCAGGCTGCTGTTCATGGAGTGTAGCAGCGTGTGCCC 300

Qy 571 GAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTC 630  
 ||||| ||||| || || || ||||| ||||| |||||  
 Db 301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy 631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTC 690  
 || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTACCTACCTGGCCCCACTGGGCCTC 420

Qy 691 ATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 421 ATGGCCATGGCCTATTTCCAGATCTTCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy 751 ACCTCAGCACTGGTGCGGAAGTGAAGCGCCCCCTCAGACCAGCTGGGGGACCTGGAGCAG 810  
 ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 481 ACCTCGGCCCTGGTGCGCAAGTGAAGCGGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy 811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy 871 CGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGC 930  
 || || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGC 660

Qy 931 TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 661 TACCTGCCCATCAGTGTCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy 991 AGTGACCGGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050  
 || ||||| || || ||||| ||||| ||||| ||||| |||||  
 Db 721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy 1051 AGCGCTGCC 1059  
 ||||| |||  
 Db 781 AGCGCCGCC 789

RESULT 15  
 US-09-119-788-1  
 ; Sequence 1, Application US/09119788

```

; Patent No. 6166193
; GENERAL INFORMATION:
;   APPLICANT: Yanagisawa, Masashi
;   TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES
;   TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SmithKline Beecham Corporation
;     STREET: 709 Swedeland Road
;     CITY: King of Prussia
;     STATE: PA
;     COUNTRY: United States of America
;     ZIP: 19406
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/119,788
;     FILING DATE: 21-JUL-1998
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/053,790
;     FILING DATE: 25-JUL-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: King, William T
;     REGISTRATION NUMBER: 30,954
;     REFERENCE/DOCKET NUMBER: GH50029
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 610-270-5515
;     TELEFAX: 610-270-5090
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1633 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: Genomic DNA
US-09-119-788-1

```

```

Query Match          43.4%; Score 554.4; DB 3; Length 1633;
Best Local Similarity 68.2%; Pred. No. 8.3e-120;
Matches 819; Conservative 0; Mismatches 366; Indels 15; Gaps 3;

```

```

Qy      80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      217 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 276

Qy      140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      277 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 336

Qy      200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      337 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 396

```



Qy		260	ACCTGTCCCTGGCTGACGTTCTCGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG	319
Db		397	ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCAGCCACACTGGTCGTGG	456
Qy		320	ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG	379
Db		457	ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCTTATCTACAGA	516
Qy		380	CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG	439
Db		517	CCGTGTCCGTGTCTGTGTCTGTCTCATCTGAGCTGTATCGCCTTGGATCGGTGGTATG	576
Qy		440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGCGGGCCCGTGGCTCCATCCTGG	499
Db		577	CAATCTGTCAACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA	636
Qy		500	GCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db		637	TCATCTGGATTGTCTCCTGCATTATAATGATTTCCTCAGGCCATCGTCATGGAGTGCAGCA	696
Qy		560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG	619
Db		697	CCGTGTTCCCAGGCTTAGCCAATAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG	756
Qy		620	CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC	679
Db		757	GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC	816
Qy		680	CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA	739
Db		817	CACTGTGTCTCATGGTGTGGCTTATCTGCAAATATTTGCAAACTCTGGTGTGACAGA	876
Qy		740	TCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGCCCCCTCAGACCAGCTGGGGG	799
Db		877	TCCCTGGAACATCATCTGTAGTTTTCAGAGAAAATGGAAGCCCC-----TGCAGCCTGTTT	930
Qy		800	ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG	859
Db		931	CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA	990
Qy		860	TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTCTGCTGGTCT	919
Db		991	TAAAGCAGATCCGAGCCAGAAGGAAAAACAGCCCGGATGTTGATGGTGTGCTTTTGGTAT	1050
Qy		920	TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCTTAAAGAGGGTGTTCGGGATGT	979
Db		1051	TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT	1110
Qy		980	TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCCTGGCTGG	1039
Db		1111	TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTACACTGGCTTG	1170
Qy		1040	TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGGCAAATTCGGGG	1099
Db		1171	TATATGCCAATAGTGTGCGAATCCAATTATTTATAATTTTCTCAGTGGAAAATTTTCGAG	1230



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 19:59:43 ; Search time 659.145 Seconds  
(without alignments)  
9829.265 Million cell updates/sec

Title: US-10-070-532-1  
Perfect score: 1278  
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgcctgcctga 1278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

8  
Result Query

No.	Score	Match	Length	DB	ID	Description
1	1274.8	99.7	1564	9	US-09-828-538-23	Sequence 23, Appl
2	1274.8	99.7	1564	15	US-10-225-567A-367	Sequence 367, App
3	1274.8	99.7	1564	16	US-10-352-684A-21	Sequence 21, Appl
4	1270	99.4	1278	11	US-09-826-509-548	Sequence 548, App
5	1207.4	94.5	1209	14	US-10-077-874-1	Sequence 1, Appli
6	1201	94.0	1209	10	US-09-393-696-1	Sequence 1, Appli
7	1085.8	85.0	1110	14	US-10-077-874-3	Sequence 3, Appli
8	1083.2	84.8	1116	14	US-10-077-874-5	Sequence 5, Appli
9	1083.2	84.8	1133	10	US-09-393-696-5	Sequence 5, Appli
10	1083	84.7	1281	9	US-09-730-931-1	Sequence 1, Appli
11	1077.8	84.3	1110	10	US-09-393-696-3	Sequence 3, Appli
12	672.2	52.6	789	15	US-10-278-087A-55	Sequence 55, Appl
13	554.4	43.4	1633	15	US-10-282-717-1	Sequence 1, Appli
14	554.4	43.4	1843	15	US-10-225-567A-369	Sequence 369, App
15	549.6	43.0	1335	11	US-09-826-509-550	Sequence 550, App
16	249.2	19.5	9785	9	US-09-961-848-1	Sequence 1, Appli
17	249.2	19.5	10453	9	US-09-828-538-21	Sequence 21, Appl
18	244	19.1	244	9	US-09-828-538-6	Sequence 6, Appli
19	227	17.8	227	9	US-09-828-538-10	Sequence 10, Appl
20	199	15.6	356	9	US-09-828-538-2	Sequence 2, Appli
21	189.4	14.8	324	9	US-09-828-538-14	Sequence 14, Appl
22	179	14.0	179	9	US-09-828-538-4	Sequence 4, Appli
23	163.2	12.8	1290	17	US-10-719-587-55	Sequence 55, Appl
24	163.2	12.8	1290	17	US-10-719-587-56	Sequence 56, Appl
25	163.2	12.8	1293	9	US-09-866-248A-7	Sequence 7, Appli
26	163.2	12.8	1293	15	US-10-225-567A-657	Sequence 657, App
27	163.2	12.8	1320	9	US-09-292-973-3	Sequence 3, Appli
28	156.2	12.2	1299	17	US-10-719-587-38	Sequence 38, Appl
29	156.2	12.2	1410	9	US-09-866-248A-1	Sequence 1, Appli
30	149.8	11.7	1532	9	US-09-292-973-1	Sequence 1, Appli
31	128.4	10.0	168575	15	US-10-178-194-1	Sequence 1, Appli
32	126	9.9	977	12	US-09-876-143-1561	Sequence 1561, Ap
33	122	9.5	122	9	US-09-828-538-12	Sequence 12, Appl
34	120.6	9.4	1174	17	US-10-611-210-9	Sequence 9, Appli
35	119	9.3	1110	14	US-10-044-592-17	Sequence 17, Appl
36	119	9.3	1110	15	US-10-278-087A-31	Sequence 31, Appl
37	119	9.3	1113	15	US-10-225-567A-244	Sequence 244, App
38	119	9.3	1152	17	US-10-611-210-10	Sequence 10, Appl
39	119	9.3	1174	17	US-10-611-210-7	Sequence 7, Appli
40	119	9.3	1331	14	US-10-044-592-73	Sequence 73, Appl
41	118.4	9.3	1173	17	US-10-611-210-6	Sequence 6, Appli
42	116	9.1	116	9	US-09-828-538-8	Sequence 8, Appli
43	115.8	9.1	1174	17	US-10-611-210-8	Sequence 8, Appli
44	107.2	8.4	669	14	US-10-044-592-70	Sequence 70, Appl
c 45	105.6	8.3	436	13	US-10-027-632-275272	Sequence 275272,

#### ALIGNMENTS

#### RESULT 1

US-09-828-538-23

; Sequence 23, Application US/09828538

; Patent No. US20010025031A1

; GENERAL INFORMATION:

; APPLICANT: Ellis, Catherine E.  
 ; APPLICANT: Kwok, Cheni  
 ; APPLICANT: Bodsworth, Nicola J.  
 ; APPLICANT: Halsey, Wendy  
 ; APPLICANT: Van Horn, Stephanie  
 ; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods  
 ; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications  
 ; FILE REFERENCE: GH-50038-C1  
 ; CURRENT APPLICATION NUMBER: US/09/828,538  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/088,624  
 ; PRIOR FILING DATE: 1998-06-08  
 ; PRIOR APPLICATION NUMBER: 60/093,726  
 ; PRIOR FILING DATE: 1998-07-22  
 ; PRIOR APPLICATION NUMBER: 09/328,014  
 ; PRIOR FILING DATE: 1999-06-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 23  
 ; LENGTH: 1564  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-09-828-538-23

Query Match 99.7%; Score 1274.8; DB 9; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	154	ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480

Db	574		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	874		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	933
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	934		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	993
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961		AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114		AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1080
Db	1174		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1233
Qy	1081		CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1234		CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1293
Qy	1141		GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200
Db	1294		GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1353
Qy	1201		TCCTTGACAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1260
Db	1354		TCCTTGACAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC	1413
Qy	1261		ACCACAGTGCTGCCCTGA	1278

Db 1414 ACCACAGTGCTGCCCTGA 1431

RESULT 2

US-10-225-567A-367

; Sequence 367, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 367

; LENGTH: 1564

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-367

Query Match 99.7%; Score 1274.8; DB 15; Length 1564;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60
          |||
Db      154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
          |||
Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
          |||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||
```

Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||

Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 |||

Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||

Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||

Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCAGATATTCCGC 720  
 |||

Db 814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCAGATATTCCGC 873

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 |||

Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 |||

Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||

Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT 960  
 |||

Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT 1113

Qy 961 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||

Db 1114 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||

Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233

Qy 1081 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||

Db 1234 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||

Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy 1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||

Db 1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32

US-10-352-684A-21

```

; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 1564
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)...(1431)
US-10-352-684A-21

```

Query Match 99.7%; Score 1274.8; DB 16; Length 1564;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
      |||
Db     154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      |||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
      |||
Db    274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
      |||
Db    334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
      |||
Db    394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
      |||
Db    454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC 420
      |||
Db    514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
      |||
Db    574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
      |||
Db    634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
      |||
Db    694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
      |||
Db    754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
      |||
Db    814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
      |||
Db    874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933
```

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||  
 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993  
 |||  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 |||  
 Qy 901 ATGGTGGTGTCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 1054 ATGGTGGTGTCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 |||  
 Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 |||  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080  
 |||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1233  
 |||  
 Qy 1081 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||  
 Db 1234 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293  
 |||  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||  
 Db 1294 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353  
 |||  
 Qy 1201 TCCTTGAGAGCCGATGCTCCGTCTCCAAATCTCTGAGCATGTGGTGTCTACCAGCGTC 1260  
 |||  
 Db 1354 TCCTTGAGAGCCGATGCTCCATCTCCAAATCTCTGAGCATGTGGTGTCTACCAGCGTC 1413  
 |||  
 Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||  
 Db 1414 ACCACAGTGCTGCCCTGA 1431  
 |||

#### RESULT 4

US-09-826-509-548

; Sequence 548, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 548  
; LENGTH: 1278  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-826-509-548

Query Match 99.4%; Score 1270; DB 11; Length 1278;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1273; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        |||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        |||
Db     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        |||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        |||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        |||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        |||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        |||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
        |||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        |||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        |||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
        |||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
```

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 |||||||||||||||||||||||||||||||||||||||||||||  
 Db 1081 CTCAGTGGCAAATTCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140  
 Qy 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 |||||||||||||||||||||||||||||||||||||||||||||  
 Db 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200  
 Qy 1201 TCCTTGAGAGCCGATGCTCCGCTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 |||||||||||||||||||  
 Db 1201 TCCTTGAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260  
 Qy 1261 ACCACAGTGCTGCCCTGA 1278  
 |||||||  
 Db 1261 ACCACAGTGCTGCCCTGA 1278

RESULT 5

US-10-077-874-1

; Sequence 1, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

```

;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/077,874
;      FILING DATE: 20-Feb-2002
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/462,509
;      FILING DATE: 05-JUNE-1995
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Wales, Michele M.
;      REGISTRATION NUMBER: 43,975
;      REFERENCE/DOCKET NUMBER: PF168P1D1
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 301-309-8504
;      TELEFAX: 301-309-8439
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 1209 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: cDNA
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 1..1209
;      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-077-874-1

```

```

Query Match          94.5%;  Score 1207.4;  DB 14;  Length 1209;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1208;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        |||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        |||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        |||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        |||
Db    241 ACCAACTACTTCATTGTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

```

Db	301	 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	 ATTGTCACCTACCTGGCCCCACTGGGCCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721	 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781	 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	 ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961	 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1080
Db	1021	 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1080
Qy	1081	CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1081	 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Qy	1141	GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200

```

Db      1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
Qy      1201 TCCTTGCGAG 1209
          ||||| ||
Db      1201 TCCTGTAG 1209

```

RESULT 6

US-09-393-696-1

```

; Sequence 1, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1209)
US-09-393-696-1

```

```

Query Match          94.0%; Score 1201; DB 10; Length 1209;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1204; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
          |||||||
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
          |||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

```



Db	301		CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721		AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Qy	841		CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Db	841		CGCGCCTTCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901		ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901		ATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGTGCCAAACCCATCATCTACAACTTC	1080
Db	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGTGCCAAACCCATCATCTACAACTTC	1080
Qy	1081		CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Db	1081		CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG	1140
Qy	1141		GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG	1200

Db 1141 GGTCCCTGCGGCTCTCTGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy 1201 TCCTTG CAG 1209

||||| ||

Db 1201 TCCTTG TAG 1209

RESULT 7

US-10-077-874-3

; Sequence 3, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1110 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1110

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-077-874-3

Query Match 85.0%; Score 1085.8; DB 14; Length 1110;

Best Local Similarity 99.8%; Pred. No. 6.6e-295;

Matches 1087; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCG	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCG	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC	840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080

Qy 1081 CTCAGTGGC 1089  
 |||  
 Db 1081 CTCAGTGGC 1089

RESULT 8

US-10-077-874-5

; Sequence 5, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

```

;           LENGTH: 1116 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;           MOLECULE TYPE: DNA (genomic)
;           FEATURE:
;             NAME/KEY: CDS
;             LOCATION: 1..1116
;           SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-077-874-5

```

```

Query Match          84.8%;  Score 1083.2;  DB 14;  Length 1116;
Best Local Similarity 99.7%;  Pred. No. 3.6e-294;
Matches 1085;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

```

```

Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGACCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080  
 Qy 1081 CTCAGTGG 1088  
 |||||||  
 Db 1081 CTCAGTGG 1088

# RESULT 9

US-09-393-696-5

; Sequence 5, Application US/09393696

; Publication No. US2003002227A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; FILE REFERENCE: PF168P2

; CURRENT APPLICATION NUMBER: US/09/393,696

; CURRENT FILING DATE: 1999-09-10

; EARLIER APPLICATION NUMBER: PCT/US95/05616

; EARLIER FILING DATE: 1995-05-05

; EARLIER APPLICATION NUMBER: US08/462,509

; EARLIER FILING DATE: 1995-06-05

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1133

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1131)  
US-09-393-696-5

Query Match 84.8%; Score 1083.2; DB 10; Length 1133;  
Best Local Similarity 99.7%; Pred. No. 3.6e-294;  
Matches 1085; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGACCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCCTGGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCCTGGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC 780
        |||||||||||||||||||||||||||||||||||||||||||||||||
```

```

Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780
Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT 960
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT 960
Qy      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1080
Qy      1081 CTCAGTGG 1088
      |||||||
Db      1081 CTCAGTGG 1088

```

RESULT 10

US-09-730-931-1

; Sequence 1, Application US/09730931

; Patent No. US20020064814A1

; GENERAL INFORMATION:

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: DOG OREXIN 1 RECEPTOR

; FILE REFERENCE: GH-70669

; CURRENT APPLICATION NUMBER: US/09/730,931

; CURRENT FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: 60/169,373

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1281

; TYPE: DNA

; ORGANISM: CANIS FAMILIARIS

US-09-730-931-1

```

Query Match      84.7%; Score 1083; DB 9; Length 1281;
Best Local Similarity 90.9%; Pred. No. 4.2e-294;
Matches 1165; Conservative 0; Mismatches 110; Indels 6; Gaps 1;

```

```

Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
      |||||||||||||||||||||||||||| ||| |||| | ||| || |||||
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGACTGGGACCCCCACCGGCGGCGGGGAGCTG 60
Qy      61 TCCCCT-----GTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGAT 114
      || || ||||||| ||||||||| ||||| || ||||||||| |||||

```



Db	61	TCTCCGTC	ACTGGTGC	CTCCCGAC	TATGAAGAC	GAGTTCC	TGCGCTAT	CTGTGGC	GCGGAT	120			
Qy	115	TATCTGT	TACCCAAA	CAGTATG	AGTGGGT	CCTCATC	GCAGCCT	ATGTGGC	TGTGTT	CGTC	174		
Db	121	TACCTGT	TACCCAAA	AGCAGT	ATGAGT	GGGTCC	TATCGCT	GCCTAC	GTGGCT	TGTGTT	CCTA	180	
Qy	175	GTGGCC	CTGGTGG	GCAACAC	GCTGGT	CTGCCT	TGGCCG	TGTGGC	GGAACC	ACCACAT	GAGG	234	
Db	181	GTGGCC	CTGGTGG	GCAACAC	GCTGGT	CTGCCT	TGGCCG	TGTGGA	GGAACC	ACCACAT	GAGG	240	
Qy	235	ACAGTC	ACCAACT	ACTTCA	TTGTCA	ACCTGT	CCCTGG	CTGACG	TTCTGG	TGACTG	CTATC	294	
Db	241	ACGGTC	ACCAACT	ATTTCA	TTGTCA	ACCTGT	CCCTGG	CTGATG	TGCTGG	TGACAG	CCATC	300	
Qy	295	TGCCTG	CCGGCC	AGCCTG	CTGGT	GACATC	ACTGAG	TCCTGG	CTGTT	CGGCCA	TGCCCT	354	
Db	301	TGCCTC	CCGGCC	AGCCTG	CTGGT	AGACAT	CCTGAG	TCCTGG	CTCTCG	GTCATA	CCCTC	360	
Qy	355	TGCAAG	GTCA	TCCCCT	ATCTAC	AGGCTG	TGCCGT	GTCAGT	GGCAGT	GCTAACT	CTCAGC	414	
Db	361	TGCAAG	GTCA	TCCCCT	ATCTAC	AGGCCG	TGTCTG	TGTCGG	TGGCAG	TGCTGAC	TCTCAGC	420	
Qy	415	TTCATC	GC	CCCTGG	ACCGCT	GGTATG	CCATCT	GCCACCC	ACTATT	GTTCA	AGAGCA	CAGCC	474
Db	421	TTCATC	GC	CCCTGG	ACCGCT	GGTATG	CCATCT	GCCACCC	GCTGTT	GTTCA	AGAGCA	CCGCC	480
Qy	475	CGGCGG	GCCCGT	GGCTCC	ATCCTG	GGCATC	TGGGCT	GTGT	CGCTGG	CCATCAT	GGTGCCC	534	
Db	481	CGGCGG	GCCCGC	AGCTCC	ATCCTG	GGCATC	TGGGCT	GTGT	CATTGG	CTGT	CATGGT	TACCT	540
Qy	535	CAGGCT	TGCAGT	CATGGA	ATGCAG	CAGTGT	GCTGC	CTGAGC	TAGCCA	AACCGC	ACACGG	CTC	594
Db	541	CAGGCT	TGCCGT	CATGGA	ATGCAG	CAGCGT	GCTCC	CTGAGC	TAGCCA	AACCGC	ACCCGC	CTC	600
Qy	595	TTCTCA	GTCTGT	GATGA	ACGCTG	GGGCA	GATGAC	CTCTAT	CCCAAG	ATCTAC	CACAGT	TGC	654
Db	601	TTCTCT	GTGTGT	GATGA	ACACTG	GGGCA	GATGAC	CTCTAT	CCCAAG	ATCTAC	CACAGT	TGC	660
Qy	655	TTCTTT	ATTGTC	ACCTAC	CTGGCC	CCACTG	GGCCTC	ATGGCC	ATGGC	CTATTT	CCAGAT	A	714
Db	661	TTCTTC	ATTGTC	ACCTAC	TTGGCC	CCACTG	GGCCTC	ATGGCC	ATGGC	CTATTT	CCAGAT	C	720
Qy	715	TTCCGC	AAAGCT	CTGGGG	CCGCCA	GATCCCC	GGCACC	ACCTCA	GCACTG	GTGCGG	AACTGG	774	
Db	721	TTCCGC	AAAGCT	CTGGGG	CCGCCA	GATCCCT	GGCACC	ACATCG	GCCCTG	GTGAGG	AACTGG	780	
Qy	775	AAGCGC	CCCCCT	CAGACC	AGCTGG	GGGGAC	CTGGAG	CAGGGC	CTGAGT	GAGAGC	CCCCAG	CCC	834
Db	781	AAGCGC	CCCCCT	CGGACC	AGCTGG	AGGACC	AGGGGC	CCGGCT	GAGCGC	GGAAC	CCCCCCC	CT	840
Qy	835	CGGGCC	CGCGCT	TTCTGG	CTGAAG	TGAAGC	AGATG	CGTGC	CACGG	AGGAAG	ACAGCC	AAG	894
Db	841	CGGGCC	CGGGCT	TT									



Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
 |||

Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC 180  
 |||

Db 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC 180

Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 |||

Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 |||

Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 |||

Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||

Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||

Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGTGGCCATCATGGTGCCCCAGGCT 540  
 |||

Db 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||

Db 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||

Db 601 CTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||

Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACCTGGAAGCGC 780  
 |||

Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACCTGGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840  
 |||

Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||

Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080

Qy 1081 CTCAGTGGC 1089  
 |||  
 Db 1081 CTCAGTGGC 1089

RESULT 12

US-10-278-087A-55

; Sequence 55, Application US/10278087A

; Publication No. US20030138817A1

; GENERAL INFORMATION:

; APPLICANT: Shuji Hinuma

; Yasuaki Ito

; Ryo Fujii

; TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
 ; Production, And Use Thereof

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwards & Angell, LLP

; STREET: 101 Federal Street

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02209

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/278,087A

; FILING DATE: 31-Jan-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/461,436

; FILING DATE: 14-DEC-1999

; APPLICATION NUMBER: 09/038,572

; FILING DATE: 11-MAR-1998

; APPLICATION NUMBER: 08/513,974

; FILING DATE: 14-SEP-1995

; APPLICATION NUMBER: PCT/JP95/01599

; FILING DATE: 10-AUG-1995

; APPLICATION NUMBER: 7-093989

; FILING DATE: 19-APR-1995

; APPLICATION NUMBER: 7-057186

```

; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-278-087A-55

```

```

Query Match          52.6%; Score 672.2; DB 15; Length 789;
Best Local Similarity 90.7%; Pred. No. 1.1e-178;
Matches 716; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```

```

Qy      271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
        || || || ||||| || ||||| ||||| ||||| ||||| ||||| ||
Db      1   GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy      331 TCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
        ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy      391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy      451 CCACTATTGTTCAAGAGCACAGCCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
        || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 CCGCTGTTGTTCAAGAGCACTGCCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy      511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241 GTGTCGCTGGCTGTCATGGTGCCCTCAGGCTGCTGTTCATGGAGTGTAGCAGCGTGTGCC 300

```



; SEQ ID NO 1  
; LENGTH: 1633  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-10-282-717-1

Query Match 43.4%; Score 554.4; DB 15; Length 1633;  
Best Local Similarity 68.2%; Pred. No. 1.8e-145;  
Matches 819; Conservative 0; Mismatches 366; Indels 15; Gaps 3;

Qy	80	ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT	139
Db	217	ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT	276
Qy	140	GGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCCCTGGTGGGCAACACGCTGG	199
Db	277	GGGTCTGATCGCCGGGTACATCATCGTGTTCGTTCGTGGCTCTCATTGGGAACGTCCTGG	336
Qy	200	TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	337	TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA	396
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG	319
Db	397	ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG	456
Qy	320	ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG	379
Db	457	ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCTTATCTACAGA	516
Qy	380	CTGTGTCCGTGTCTAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG	439
Db	517	CCGTGTCCGTGTCTGTGTCTGTCTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG	576
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGGGGGGCCCGTGGCTCCATCCTGG	499
Db	577	CAATCTGTACCCCTTGTATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTTGTCA	636
Qy	500	GCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	637	TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA	696
Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG	619
Db	697	CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG	756
Qy	620	CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC	679
Db	757	GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC	816
Qy	680	CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCCAGA	739
Db	817	CACTGTGTCTCATGGTGTGGCTTATCTGCAAATATTTTCGCAAACCTCTGGTGTGACAGA	876
Qy	740	TCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGCCCCCTCAGACCAGCTGGGGG	799
Db	877	TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC-----TGCAGCCTGTTT	930

Qy 800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCCGCGCCTTCCTGGCTGAAG 859  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 931 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA 990  
 Qy 860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGGCTGCTGGTCT 919  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 991 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1050  
 Qy 920 TCGCCCTCTGCTACCTGCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1051 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1110  
 Qy 980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCGCTTCACCTTCTCCCACTGGCTGG 1039  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1111 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1170  
 Qy 1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGGCAAATTCGGG 1099  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1171 TATATGCCAATAGTGCTGCGAATCAATTATTTATAATTTTCTCAGTGGAAAATTTTCGAG 1230  
 Qy 1100 AGCAGTTTAAGGCTGCCTTCTC---CTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTC 1156  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1231 AGGAATTTAAAGCTGCGTTTCTTGCTGTTGCCTTGGAGTTCACCATCGCCAGGAGGATC 1290  
 Qy 1157 TGAAGGCCCTTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCTTGCAGAGCCGAT 1216  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1291 GGCTCACCAGGGGACGAAGTAGCACAGAGAGCCGGAAGTCCTTGACCACTCAAATCAGCA 1350  
 Qy 1217 GCT-----CCGTCTCCAAAATCTCTGAGCATGTGGTGGCTCACCAGCGTCACCACAGTGC 1270  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1351 ACTTTGATAACATATCAAACTTTCTGAGCAAGTTGTGCTCACTAGCATAAGCACACTCC 1410

# RESULT 14

US-10-225-567A-369

; Sequence 369, Application US/10225567A

; Publication No. US20030113798A1

## ; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 369

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-369



Query Match 43.4%; Score 554.4; DB 15; Length 1843;  
Best Local Similarity 68.2%; Pred. No. 1.8e-145;  
Matches 819; Conservative 0; Mismatches 366; Indels 15; Gaps 3;

Qy		80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAACAGTATGAGT	139
Db	428	ACGACGAGGAATTCTCTGC GG TACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT	487
Qy	140	GGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCCCTGGTGGGCAACACGCTGG	199
Db	488	GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTTCGTGGCTCTCATTGGGAACGTCCTGG	547
Qy	200	TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	548	TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA	607
Qy	260	ACCTGTCCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG	319
Db	608	ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG	667
Qy	320	ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCATCTACAGG	379
Db	668	ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA	727
Qy	380	CTGTGTCCGTGT CAGTGGCAGTGCTA ACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG	439
Db	728	CCGTGTCGGTGTCTGTGTCTGT CCTCACACT'GAGCTGTATCGCCTTGGATCGGTGGTATG	787
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCCGGCGGGCCCGTGGCTCCATCCTGG	499
Db	788	CAATCTGTCACCCCTTTGATGTTTAAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA	847
Qy	500	GCATCTGGGCTGTGT CGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	848	TCATCTGGATTGTCTCCTGCATTATAATGATTCTCAGGCCATCGTCATGGAGTGCAGCA	907
Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG	619
Db	908	CCGTGTTCCAGGCTTAGCCAATAAACACCCCTCTTTACGGTGTGTGATGAGCGCTGGG	967
Qy	620	CAGATGACCTCTATCCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC	679
Db	968	GTGGTGAAATTTATCCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC	1027
Qy	680	CACTGGGCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA	739
Db	1028	CACTGTGTCTCATGGTGTGGCTTATCTGCAAATATTTGCAAACCTCTGGTGTGACAGA	1087
Qy	740	TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCTCAGACCAGCTGGGGG	799
Db	1088	TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC-----TGCAGCCTGTTT	1141
Qy	800	ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCGCGCCTTCTGGCTGAAG	859
Db	1142	CACAGCCTCGAGGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA	1201



Matches 816; Conservative 0; Mismatches 369; Indels 15; Gaps 3;

```
Qy      80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     104 ACGACGAGGAATTCTCGGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 163

Qy     140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCCCTGGTGGGCAACACGCTGG 199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     164 GGGTCCTGATCGCCGGGTACATCATCGTGTTTCGTTCGTGGCTCTCATTGGGAACGTCCTGG 223

Qy     200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     224 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 283

Qy     260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     284 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 343

Qy     320 ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCTATCTACAGG 379
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     344 ATATCACTGAGACCTGGTTTTTTTGGACAGTCCCTTTGCAAAGTGATTCTTATCTACAGA 403

Qy     380 CTGTGTCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     404 CCGTGTCCGGTGTCTGTGTCTGTCTCACACTGAGCTGTATCGCCTTGGATCCGTGGTATG 463

Qy     440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     464 CAATCTGTCAACCTTTGATGTTTAAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 523

Qy     500 GCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     524 TCATCTGGATTGTCTCCTGCATTATAATGATTCTCAGGCCATCGTCATGGAGTGCAGCA 583

Qy     560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     584 CCGTGTTCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 643

Qy     620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC 679
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     644 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 703

Qy     680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     704 CACTGTGTCTCATGGTGTGGCTTATCTGCAAATATTTGCAAACCTCTGGTGTGACAGA 763

Qy     740 TCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGCCCTCAGACCAGCTGGGGG 799
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     764 TCCCTGGAACATCATCTGTAGTTTACAGAGAAAATGGAAGCCCC-----TGCAGCCTGTTT 817

Qy     800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGGCCTTCCTGGCTGAAG 859
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     818 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 877

Qy     860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGCTGCT 919
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     878 TAAAGCAGATCCGAGCCAGAAGGAAAACAAAACGGATGTTGATGGTTGTGCTTTTGGTAT 937
```

Qy 920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 938 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 997  
  
 Qy 980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 998 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1057  
  
 Qy 1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGGCAAATTCCGGG 1099  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1058 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGAAAATTTTCGAG 1117  
  
 Qy 1100 AGCAGTTTTAAGGCTGCCTTCTC---CTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTC 1156  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1118 AGGAATTTAAAGCTGCGTTTTCTTGCTGTTGCCTTGAGATTACCATCGCCAGGAGGATC 1177  
  
 Qy 1157 TGAAGGCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGACAGAGCCGAT 1216  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1178 GGCTCACCAGGGGACGAAGTAGCACAGAGAGCCGGAAGTCCTTGACCACTCAAATCAGCA 1237  
  
 Qy 1217 GCT-----CCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGC 1270  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1238 ACTTTGATAACATATCAAACTTTCTGAGCAAGTTGTGCTCACTAGCATAAGCACACTCC 1297

Search completed: October 16, 2004, 03:40:39  
 Job time : 663.145 secs